

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lal, Preeti  
Hillman, Jennifer L.  
Corley, Neil C.  
Guegler, Karl J.  
Baugh, Mariah  
Sather, Susan  
Shah, Purvi

(ii) TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS

(iii) NUMBER OF SEQUENCES:154

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
(B) STREET: 3174 PORTER DRIVE  
(C) CITY: PALO ALTO  
(D) STATE: CALIFORNIA  
(E) COUNTRY: USA  
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: TO BE ASSIGNED  
(B) FILING DATE: HERewith  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: BILLINGS, LUCY J.  
(B) REGISTRATION NUMBER: 36,749  
(C) REFERENCE/DOCKET NUMBER:PF-0459 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650) 855-0555  
(B) TELEFAX: (650) 845-4166

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

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(A) LIBRARY: HEARNOT01

(B) CLONE: 305841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 :

Met	Ala	Ala	Thr	Leu	Gly	Pro	Leu	Gly	Ser	Trp	Gln	Gln	Trp	Arg	
				5					10					15	
Arg	Cys	Leu	Ser	Ala	Arg	Asp	Gly	Ser	Arg	Met	Leu	Leu	Leu	Leu	
				20					25					30	
Leu	Leu	Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val	Gly	Ala	Gly	
				35					40					45	
Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro	
				50					55					60	
Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met	
				65					70					75	
Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp	
				80					85					90	
Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe	
				95					100					105	
Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln	
				110					115					120	
Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr	
				125					130					135	
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys	
				140					145					150	
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu	
				155					160					165	
Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn	
				170					175					180	
Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr	
				185					190					195	
Glu	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp	
				200					205					210	
Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met	
				215					220					225	
Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val	
				230					235					240	
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser	
				245					250					255	
Ile	Thr	Gly	Asp	Leu	Ser	Asp	Asn	His	Asp	Val	Ile	Ser	Leu	Lys	
				260					265					270	
Leu	Phe	Glu	Leu	Thr	Val	Glu	Arg	Thr	Pro	Glu	Glu	Glu	Lys	Leu	
				275					280					285	
His	Arg	Asp	Val	Phe	Leu	Pro	Ser	Val	Asp	Asn	Met	Lys	Leu	Pro	
				290					295					300	
Glu	Met	Thr	Ala	Pro	Leu	Pro	Pro	Leu	Ser	Gly	Leu	Ala	Leu	Phe	
				305					310					315	
Leu	Ile	Val	Phe	Phe	Ser	Leu	Val	Phe	Ser	Val	Phe	Ala	Ile	Val	
				320					325					330	
Ile	Gly	Ile	Ile	Leu	Tyr	Asn	Lys	Trp	Gln	Glu	Gln	Ser	Arg	Lys	
				335					340					345	
Arg	Phe	Tyr													

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: EOSIHET02  
(B) CLONE: 322866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2 :

Met	Gly	Met	Ser	Ser	Leu	Lys	Leu	Leu	Lys	Tyr	Val	Leu	Phe	Phe	5	10	15
Phe	Asn	Leu	Leu	Phe	Trp	Ile	Cys	Gly	Cys	Cys	Ile	Leu	Gly	Phe	20	25	30
Gly	Ile	Tyr	Leu	Leu	Ile	His	Asn	Asn	Phe	Gly	Val	Leu	Phe	His	35	40	45
Asn	Leu	Pro	Ser	Leu	Thr	Leu	Gly	Asn	Val	Phe	Val	Ile	Val	Gly	50	55	60
Ser	Ile	Ile	Met	Val	Val	Ala	Phe	Leu	Gly	Cys	Met	Gly	Ser	Ile	65	70	75
Lys	Glu	Asn	Lys	Cys	Leu	Leu	Met	Ser	Phe	Phe	Ile	Leu	Leu	Leu	80	85	90
Ile	Ile	Leu	Leu	Ala	Glu	Val	Thr	Leu	Ala	Ile	Leu	Leu	Phe	Val	95	100	105
Tyr	Glu	Gln	Lys	Leu	Asn	Glu	Tyr	Val	Ala	Lys	Gly	Leu	Thr	Asp	110	115	120
Ser	Ile	His	Arg	Tyr	His	Ser	Asp	Asn	Ser	Thr	Lys	Ala	Ala	Trp	125	130	135
Asp	Ser	Ile	Gln	Ser	Phe	Leu	Gln	Cys	Cys	Gly	Ile	Asn	Gly	Thr	140	145	150
Ser	Asp	Leu	Asp	Ser	Gly	Ser	Pro	Ala	Ser	Cys	Pro	Ser	Asp	Arg	155	160	165
Lys	Val	Glu	Gly	Cys	Tyr	Ala	Lys	Glu	Asp	Phe	Gly	Phe	Ile	Gln	170	175	180
Phe	Pro	Val	Tyr	Arg	Asn	His	His	His	Leu	Cys	Met	Cys	Asp		185	190	

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 342 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: BEPINOT01  
(B) CLONE: 546656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3 :

Met	Ser	Leu	His	Gly	Lys	Arg	Lys	Glu	Ile	Tyr	Lys	Tyr	Glu	Ala	5	10	15
Pro	Trp	Thr	Val	Tyr	Ala	Met	Asn	Trp	Ser	Val	Arg	Pro	Asp	Lys	20	25	30
Arg	Phe	Arg	Leu	Ala	Leu	Gly	Ser	Phe	Val	Glu	Glu	Tyr	Asn	Asn	35	40	45
Lys	Val	Gln	Leu	Val	Gly	Leu	Asp	Glu	Glu	Ser	Ser	Glu	Phe	Ile	50	55	60

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Cys	Arg	Asn	Thr	Phe	Asp	His	Pro	Tyr	Pro	Thr	Thr	Lys	Leu	Met	
				65					70					75	
Trp	Ile	Pro	Asp	Thr	Lys	Gly	Val	Tyr	Pro	Asp	Leu	Leu	Ala	Thr	
				80					85					90	
Ser	Gly	Asp	Tyr	Leu	Arg	Val	Trp	Arg	Val	Gly	Glu	Thr	Glu	Thr	
				95					100					105	
Arg	Leu	Glu	Cys	Leu	Leu	Asn	Asn	Asn	Lys	Asn	Ser	Asp	Phe	Cys	
				110					115					120	
Ala	Pro	Leu	Thr	Ser	Phe	Asp	Trp	Asn	Glu	Val	Asp	Pro	Tyr	Leu	
				125					130					135	
Leu	Gly	Thr	Ser	Ser	Ile	Asp	Thr	Thr	Cys	Thr	Ile	Trp	Gly	Leu	
				140					145					150	
Glu	Thr	Gly	Gln	Val	Leu	Gly	Arg	Val	Asn	Leu	Val	Ser	Gly	His	
				155					160					165	
Val	Lys	Thr	Gln	Leu	Ile	Ala	His	Asp	Lys	Glu	Val	Tyr	Asp	Ile	
				170					175					180	
Ala	Phe	Ser	Arg	Ala	Gly	Gly	Gly	Arg	Asp	Met	Phe	Ala	Ser	Val	
				185					190					195	
Gly	Ala	Asp	Gly	Ser	Val	Arg	Met	Phe	Asp	Leu	Arg	His	Leu	Glu	
				200					205					210	
His	Ser	Thr	Ile	Ile	Tyr	Glu	Asp	Pro	Gln	His	His	Pro	Leu	Leu	
				215					220					225	
Arg	Leu	Cys	Trp	Asn	Lys	Gln	Asp	Pro	Asn	Tyr	Leu	Ala	Thr	Met	
				230					235					240	
Ala	Met	Asp	Gly	Met	Glu	Val	Val	Ile	Leu	Asp	Val	Arg	Val	Pro	
				245					250					255	
Cys	Thr	Pro	Val	Ala	Arg	Leu	Asn	Asn	His	Arg	Ala	Cys	Val	Asn	
				260					265					270	
Gly	Ile	Ala	Trp	Ala	Pro	His	Ser	Ser	Cys	His	Ile	Cys	Thr	Ala	
				275					280					285	
Ala	Asp	Asp	His	Gln	Ala	Leu	Ile	Trp	Asp	Ile	Gln	Gln	Met	Pro	
				290					295					300	
Arg	Ala	Ile	Glu	Asp	Pro	Ile	Leu	Ala	Tyr	Thr	Ala	Glu	Gly	Glu	
				305					310					315	
Ile	Asn	Asn	Val	Gln	Trp	Ala	Ser	Thr	Gln	Pro	Asp	Trp	Ile	Ala	
				320					325					330	
Ile	Cys	Tyr	Asn	Asn	Cys	Leu	Glu	Ile	Leu	Arg	Val				
				335					340						

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SYNORAT03
- (B) CLONE: 693453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4 :

Met	Glu	Glu	Leu	Asp	Gly	Glu	Pro	Thr	Val	Thr	Leu	Ile	Pro	Gly	
				5					10					15	
Val	Asn	Ser	Lys	Lys	Asn	Gln	Met	Tyr	Phe	Asp	Trp	Gly	Pro	Gly	
				20					25					30	
Glu	Met	Leu	Val	Cys	Glu	Thr	Ser	Phe	Asn	Lys	Lys	Glu	Lys	Ser	

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	35		40		45
Glu Met Val Pro Ser	Cys Pro Phe Ile Tyr	Ile Ile Arg Lys Asp			
Val Asp Val Tyr Ser	Gln Ile Leu Arg Lys	Leu Phe Asn Glu Ser			
His Gly Ile Phe Leu	Gly Leu Gln Arg Ile	Asp Glu Glu Leu Thr			
Gly Lys Ser Arg Lys	Ser Gln Leu Val Arg	Val Ser Lys Asn Tyr			
Arg Ser Val Ile Arg	Ala Cys Met Glu	Glu Met His Gln Val Ala			
Ile Ala Ala Lys Asp	Pro Ala Asn Gly Arg	Gln Phe Ser Ser Gln			
Val Ser Ile Leu Ser	Ala Met Glu Leu Ile	Trp Asn Leu Cys Glu			
Ile Leu Phe Ile Glu	Val Ala Pro Ala Gly	Pro Leu Leu Leu His			
Leu Leu Asp Trp Val	Arg Leu His Val Cys	Glu Val Asp Ser Leu			
Ser Ala Asp Val Leu	Gly Ser Glu Asn Pro	Ser Lys His Asp Ser			
Phe Trp Asn Leu Val	Thr Ile Leu Val Leu	Gln Gly Arg Leu Asp			
Glu Ala Arg Gln Met	Leu Ser Lys Glu Ala	Asp Ala Ser Pro Ala			
Ser Ala Gly Ile Cys	Arg Ile Met Gly Asp	Leu Met Arg Thr Met			
Pro Ile Leu Ser Pro	Gly Asn Thr Gln Thr	Leu Thr Glu Leu Glu			
Leu Lys Trp Gln His	Trp His Glu Glu Cys	Glu Arg Tyr Leu Gln			
Asp Ser Thr Phe Ala	Thr Ser Pro His Leu	Glu Ser Leu Leu Lys			
Ile Met Leu Gly Asp	Glu Ala Ala Leu Leu	Glu Gln Lys Glu Leu			
Leu Ser Asn Trp Tyr	His Phe Leu Val Thr	Arg Leu Leu Tyr Ser			
Asn Pro Thr Val Lys	Pro Ile Asp Leu His	Tyr Tyr Ala Gln Ser			
Ser Leu Asp Leu Phe	Leu Gly Gly Glu Ser	Ser Pro Glu Pro Leu			
Asp Asn Ile Leu Leu	Ala Ala Phe Glu Phe	Asp Ile His Gln Val			
Ile Lys Glu Cys Ser	Ile Ala Leu Ser Asn	Trp Trp Phe Val Ala			
His Leu Thr Asp Leu	Leu Asp His Cys Lys	Leu Leu Gln Ser His			
Asn Leu Tyr Phe Gly	Ser Asn Met Arg Glu	Phe Leu Leu Leu Glu			
Tyr Ala Ser Gly Leu	Phe Ala His Pro Ser	Leu Trp Gln Leu Gly			
Val Asp Tyr Phe Asp	Tyr Cys Pro Glu Leu	Gly Arg Val Ser Leu			
Glu Leu His Ile Glu	Arg Ile Pro Leu Asn	Thr Glu Gln Lys Ala			
Leu Lys Val Leu Arg	Ile Cys Glu Gln Arg	Gln Met Thr Glu Gln			
Val Arg Ser Ile Cys	Lys Ile Leu Ala Met	Lys Ala Val Arg Asn			
Asn Arg Leu Gly Ser	Ala Leu Ser Trp Ser	Ile Arg Ala Lys Asp			

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Ala	Ala	Phe	Ala	Thr	Leu	Val	Ser	Asp	Arg	Phe	Leu	Arg	Asp	Tyr
				500					505					510
Cys	Glu	Arg	Gly	Cys	Phe	Ser	Asp	Leu	Asp	Leu	Ile	Asp	Asn	Leu
				515					520					525
Gly	Pro	Ala	Met	Met	Leu	Ser	Asp	Arg	Leu	Thr	Phe	Leu	Gly	Lys
				530					535					540
Tyr	Arg	Glu	Phe	His	Arg	Met	Tyr	Gly	Glu	Lys	Arg	Phe	Ala	Asp
				545					550					555
Ala	Ala	Ser	Leu	Leu	Leu	Ser	Leu	Met	Thr	Ser	Arg	Ile	Ala	Pro
				560					565					570
Arg	Ser	Phe	Trp	Met	Thr	Leu	Leu	Thr	Asp	Ala	Leu	Pro	Leu	Leu
				575					580					585
Glu	Gln	Lys	Gln	Val	Ile	Phe	Ser	Ala	Glu	Gln	Thr	Tyr	Glu	Leu
				590					595					600
Met	Arg	Cys	Leu	Glu	Asp	Leu	Thr	Ser	Arg	Arg	Pro	Val	His	Gly
				605					610					615
Glu	Ser	Asp	Thr	Glu	Gln	Leu	Gln	Asp	Asp	Asp	Ile	Glu	Thr	Thr
				620					625					630
Lys	Val	Glu	Met	Leu	Arg	Leu	Ser	Leu	Ala	Arg	Asn	Leu	Ala	Arg
				635					640					645
Ala	Ile	Ile	Arg	Glu	Gly	Ser	Leu	Glu	Gly	Ser				
				650					655					

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT03
- (B) CLONE: 866885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5 :

Met	Ala	Pro	Asp	Pro	Trp	Phe	Ser	Thr	Tyr	Asp	Ser	Thr	Cys	Gln
				5					10					15
Ile	Ala	Gln	Glu	Ile	Ala	Glu	Lys	Ile	Gln	Gln	Arg	Asn	Gln	Tyr
				20					25					30
Glu	Arg	Lys	Gly	Glu	Lys	Ala	Pro	Lys	Leu	Thr	Val	Thr	Ile	Arg
				35					40					45
Ala	Leu	Leu	Gln	Asn	Leu	Lys	Glu	Lys	Ile	Ala	Leu	Leu	Lys	Asp
				50					55					60
Leu	Leu	Leu	Arg	Ala	Val	Ser	Thr	His	Gln	Ile	Thr	Gln	Leu	Glu
				65					70					75
Gly	Asp	Arg	Arg	Gln	Asn	Leu	Leu	Asp	Asp	Leu	Val	Thr	Arg	Glu
				80					85					90
Arg	Leu	Leu	Leu	Ala	Ser	Phe	Lys	Asn	Glu	Gly	Ala	Glu	Pro	Asp
				95					100					105
Leu	Ile	Arg	Ser	Ser	Leu	Met	Ser	Glu	Glu	Ala	Lys	Arg	Gly	Ala
				110					115					120
Pro	Asn	Pro	Trp	Leu	Phe	Glu	Glu	Pro	Glu	Glu	Thr	Arg	Gly	Leu
				125					130					135
Gly	Phe	Asp	Glu	Ile	Arg	Gln	Gln	Gln	Gln	Lys	Ile	Ile	Gln	Glu
				140					145					150
Gln	Asp	Ala	Gly	Leu	Asp	Ala	Leu	Ser	Ser	Ile	Ile	Ser	Arg	Gln

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Lys	Gln	Met	Gly	155	Gln	Glu	Ile	Gly	Asn	160	Glu	Leu	Asp	Glu	Gln	Asn	165
				170						175							180
Glu	Ile	Ile	Asp	185	Asp	Leu	Ala	Asn	Leu	190	Val	Glu	Asn	Thr	Asp	Glu	195
Lys	Leu	Arg	Asn	200	Glu	Thr	Arg	Arg	Val	205	Asn	Met	Val	Asp	Arg	Lys	210
Ser	Ala	Ser	Cys	215	Gly	Met	Ile	Met	Val	220	Ile	Leu	Leu	Leu	Leu	Val	225
Ala	Ile	Val	Val	230	Val	Ala	Val	Trp	Pro	235	Thr	Asn					

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: LUNGNOT03

(B) CLONE: 1242271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6 :

Met	Leu	Leu	Asp	Thr	Val	Gln	Lys	Val	Phe	Gln	Lys	Met	Leu	Glu			
				5					10					15			
Cys	Ile	Ala	Arg	Ser	Phe	Arg	Lys	Gln	Pro	Glu	Glu	Gly	Leu	Arg			
				20					25					30			
Leu	Leu	Tyr	Ser	Val	Gln	Arg	Pro	Leu	His	Glu	Phe	Ile	Thr	Ala			
				35					40					45			
Val	Gln	Ser	Arg	His	Thr	Asp	Thr	Pro	Val	His	Arg	Gly	Val	Leu			
				50					55					60			
Ser	Thr	Leu	Ile	Ala	Gly	Pro	Val	Val	Glu	Ile	Ser	His	Gln	Leu			
				65					70					75			
Arg	Lys	Val	Ser	Asp	Val	Glu	Glu	Leu	Thr	Pro	Pro	Glu	His	Leu			
				80					85					90			
Ser	Asp	Leu	Pro	Pro	Phe	Ser	Arg	Cys	Leu	Ile	Gly	Ile	Ile	Ile			
				95					100					105			
Lys	Ser	Ser	Asn	Val	Val	Arg	Ser	Phe	Leu	Asp	Glu	Leu	Lys	Ala			
				110					115					120			
Cys	Val	Ala	Ser	Asn	Asp	Ile	Glu	Gly	Ile	Val	Cys	Leu	Thr	Ala			
				125					130					135			
Ala	Val	His	Ile	Ile	Leu	Val	Ile	Asn	Ala	Gly	Lys	His	Lys	Ser			
				140					145					150			
Ser	Lys	Val	Arg	Glu	Val	Ala	Ala	Thr	Val	His	Arg	Lys	Leu	Lys			
				155					160					165			
Thr	Phe	Met	Glu	Ile	Thr	Leu	Glu	Glu	Asp	Ser	Ile	Glu	Arg	Phe			
				170					175					180			
Leu	Tyr	Glu	Ser	Ser	Ser	Arg	Thr	Leu	Gly	Glu	Leu	Leu	Asn	Ser			
				185					190					195			

## (2) INFORMATION FOR SEQ ID NO: 7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGFET03
- (B) CLONE: 1255027

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7 :

Met	Thr	Lys	Thr	Asp	Glu	Thr	Thr	Leu	Val	Ala	Ser	Trp	Glu	Thr	5	10	15
Arg	Glu	Lys	Thr	Ala	Lys	Thr	Thr	Leu	Phe	Leu	Pro	Leu	Glu	Phe	20	25	30
Trp	Ser	Tyr	Lys	Ala	Glu	Val	Pro	His	Leu	Pro	Glu	Leu	Ala	Tyr	35	40	45
Ser	Ala	Arg	Ser	Lys	Met	Ala	Glu	Leu	Asn	Thr	His	Val	Asn	Val	50	55	60
Lys	Glu	Lys	Ile	Tyr	Ala	Val	Arg	Ser	Val	Val	Pro	Asn	Lys	Ser	65	70	75
Asn	Asn	Glu	Ile	Val	Leu	Val	Leu	Gln	Gln	Phe	Asp	Phe	Asn	Val	80	85	90
Asp	Lys	Ala	Val	Gln	Ala	Phe	Val	Asp	Gly	Ser	Ala	Ile	Gln	Val	95	100	105
Leu	Lys	Glu	Trp	Asn	Met	Thr	Gly	Lys	Lys	Lys	Asn	Asn	Lys	Arg	110	115	120
Lys	Arg	Ser	Lys	Ser	Lys	Gln	His	Gln	Gly	Asn	Lys	Asp	Ala	Lys	125	130	135
Asp	Lys	Val	Glu	Arg	Pro	Glu	Ala	Gly	Pro	Leu	Gln	Pro	Gln	Pro	140	145	150
Pro	Gln	Ile	Gln	Asn	Gly	Pro	Met	Asn	Gly	Cys	Glu	Lys	Asp	Ser	155	160	165
Ser	Ser	Thr	Asp	Ser	Ala	Asn	Glu	Lys	Pro	Ala	Leu	Ile	Pro	Arg	170	175	180
Glu	Lys	Lys	Ile	Ser	Ile	Leu	Glu	Glu	Pro	Ser	Lys	Ala	Leu	Arg	185	190	195
Gly	Val	Thr	Glu	Gly	Asn	Arg	Leu	Leu	Gln	Gln	Lys	Leu	Ser	Leu	200	205	210
Asp	Gly	Asn	Pro	Lys	Pro	Ile	His	Gly	Thr	Thr	Glu	Arg	Ser	Asp	215	220	225
Gly	Leu	Gln	Trp	Ser	Ala	Glu	Gln	Pro	Cys	Asn	Pro	Ser	Lys	Pro	230	235	240
Lys	Ala	Lys	Thr	Ser	Pro	Val	Lys	Ser	Asn	Thr	Pro	Ala	Ala	His	245	250	255
Leu	Glu	Ile	Lys	Pro	Asp	Glu	Leu	Ala	Lys	Lys	Arg	Gly	Pro	Asn	260	265	270
Ile	Glu	Lys	Ser	Val	Lys	Asp	Leu	Gln	Arg	Cys	Thr	Val	Ser	Leu	275	280	285
Thr	Arg	Tyr	Arg	Val	Met	Ile	Lys	Glu	Glu	Val	Asp	Ser	Ser	Val	290	295	300
Lys	Lys	Ile	Lys	Ala	Ala	Phe	Ala	Glu	Leu	His	Asn	Cys	Ile	Ile	305	310	315
Asp	Lys	Glu	Val	Ser	Leu	Met	Ala	Glu	Met	Asp	Lys	Val	Lys	Glu	320	325	330
Glu	Ala	Met	Glu	Ile	Leu	Thr	Ala	Arg	Gln	Lys	Lys	Ala	Glu	Glu	335	340	345



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Leu	Lys	Arg	Leu	Thr	Asp	Leu	Ala	Ser	Gln	Met	Ala	Glu	Met	Gln
				350					355					360
Leu	Ala	Glu	Leu	Arg	Ala	Glu	Ile	Lys	His	Phe	Val	Ser	Glu	Arg
				365					370					375
Lys	Tyr	Asp	Glu	Glu	Leu	Gly	Lys	Ala	Ala	Arg	Phe	Ser	Cys	Asp
				380					385					390
Ile	Glu	Gln	Leu	Lys	Ala	Gln	Ile	Met	Leu	Cys	Gly	Glu	Ile	Thr
				395					400					405
His	Pro	Lys	Asn	Asn	Tyr	Ser	Ser	Arg	Thr	Pro	Cys	Ser	Ser	Leu
				410					415					420
Leu	Pro	Leu	Leu	Asn	Ala	His	Ala	Ala	Thr	Ser	Gly	Lys	Gln	Ser
				425					430					435
Asn	Phe	Ser	Arg	Lys	Ser	Ser	Thr	His	Asn	Lys	Pro	Ser	Glu	Gly
				440					445					450
Lys	Ala	Ala	Asn	Pro	Lys	Met	Val	Ser	Ser	Leu	Pro	Ser	Thr	Ala
				455					460					465
Asp	Pro	Ser	His	Gln	Thr	Met	Pro	Ala	Asn	Lys	Gln	Asn	Gly	Ser
				470					475					480
Ser	Asn	Gln	Arg	Arg	Arg	Phe	Asn	Pro	Gln	Tyr	His	Asn	Asn	Arg
				485					490					495
Leu	Asn	Gly	Pro	Ala	Lys	Ser	Gln	Gly	Ser	Gly	Asn	Glu	Ala	Glu
				500					505					510
Pro	Leu	Gly	Lys	Gly	Asn	Ser	Arg	His	Glu	His	Arg	Arg	Gln	Pro
				515					520					525
His	Asn	Gly	Phe	Arg	Pro	Lys	Asn	Lys	Gly	Gly	Ala	Lys	Asn	Gln
				530					535					540
Glu	Ala	Ser	Leu	Gly	Met	Lys	Thr	Pro	Glu	Ala	Pro	Ala	His	Ser
				545					550					555
Glu	Lys	Pro	Arg	Arg	Arg	Gln	His	Ala	Ala	Asp	Thr	Ser	Glu	Ala
				560					565					570
Arg	Pro	Phe	Arg	Gly	Ser	Val	Gly	Arg	Val	Ser	Gln	Cys	Asn	Leu
				575					580					585
Cys	Pro	Thr	Arg	Ile	Glu	Val	Ser	Thr	Asp	Ala	Ala	Val	Leu	Ser
				590					595					600
Val	Pro	Ala	Val	Thr	Leu	Val	Ala							
				605										

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TESTTUT02
- (B) CLONE: 1273453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8 :

Met	Val	Ile	Ser	Trp	His	Leu	Ala	Ser	Asp	Met	Asp	Cys	Val	Val
				5					10					15
Thr	Leu	Thr	Thr	Asp	Ala	Ala	Arg	Arg	Ile	Tyr	Asp	Glu	Thr	Gln
				20					25					30
Gly	Arg	Gln	Gln	Val	Leu	Pro	Leu	Asp	Ser	Ile	Tyr	Lys	Lys	Thr
				35					40					45
Leu	Pro	Asp	Trp	Lys	Arg	Ser	Leu	Pro	His	Phe	Arg	Asn	Gly	Lys

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Leu	Tyr	Phe	Lys	Pro	Ile	Gly	Asp	Pro	Val	Phe	Ala	Arg	Asp	Leu	50	55	60
				65					70								75
Leu	Thr	Phe	Pro	Asp	Asn	Val	Glu	His	Cys	Glu	Thr	Val	Phe	Gly	80	85	90
Met	Leu	Leu	Gly	Asp	Thr	Ile	Ile	Leu	Asp	Asn	Leu	Asp	Ala	Ala	95	100	105
Asn	His	Tyr	Arg	Lys	Glu	Val	Val	Lys	Ile	Thr	His	Cys	Pro	Thr	110	115	120
Leu	Leu	Thr	Arg	Asp	Gly	Asp	Arg	Ile	Arg	Ser	Asn	Gly	Lys	Phe	125	130	135
Gly	Gly	Leu	Gln	Asn	Lys	Ala	Pro	Pro	Met	Asp	Lys	Leu	Arg	Gly	140	145	150
Met	Val	Phe	Gly	Ala	Pro	Val	Pro	Lys	Gln	Cys	Leu	Ile	Leu	Gly	155	160	165
Glu	Gln	Ile	Asp	Leu	Leu	Gln	Gln	Tyr	Arg	Ser	Ala	Val	Cys	Lys	170	175	180
Leu	Asp	Ser	Val	Asn	Lys	Asp	Leu	Asn	Ser	Gln	Leu	Glu	Tyr	Leu	185	190	195
Arg	Thr	Pro	Asp	Met	Arg	Lys	Lys	Lys	Gln	Glu	Leu	Asp	Glu	His	200	205	210
Glu	Lys	Asn	Leu	Lys	Leu	Ile	Glu	Glu	Lys	Leu	Gly	Met	Thr	Pro	215	220	225
Ile	Arg	Lys	Cys	Asn	Asp	Ser	Leu	Arg	His	Ser	Pro	Lys	Val	Glu	230	235	240
Thr	Thr	Asp	Cys	Pro	Val	Pro	Pro	Lys	Arg	Met	Arg	Arg	Glu	Ala	245	250	255
Thr	Arg	Gln	Asn	Arg	Ile	Ile	Thr	Lys	Thr	Asp	Val				260	265	

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TESTTUT02
- (B) CLONE: 1275261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9 :

Met	Val	Met	Arg	Pro	Leu	Trp	Ser	Leu	Leu	Leu	Trp	Glu	Ala	Leu	5	10	15
Leu	Pro	Ile	Thr	Val	Thr	Gly	Ala	Gln	Val	Leu	Ser	Lys	Val	Gly	20	25	30
Gly	Ser	Val	Leu	Leu	Val	Ala	Ala	Arg	Pro	Pro	Gly	Phe	Gln	Val	35	40	45
Arg	Glu	Ala	Ile	Trp	Arg	Ser	Leu	Trp	Pro	Ser	Glu	Glu	Leu	Leu	50	55	60
Ala	Thr	Phe	Phe	Arg	Gly	Ser	Leu	Glu	Thr	Leu	Tyr	His	Ser	Arg	65	70	75
Phe	Leu	Gly	Arg	Ala	Gln	Leu	His	Ser	Asn	Leu	Ser	Leu	Glu	Leu	80	85	90
Gly	Pro	Leu	Glu	Ser	Gly	Asp	Ser	Gly	Asn	Phe	Ser	Val	Leu	Met	95	100	105

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Val	Asp	Thr	Arg	Gly	Gln	Pro	Trp	Thr	Gln	Thr	Leu	Gln	Leu	Lys
				110					115					120
Val	Tyr	Asp	Ala	Val	Pro	Arg	Pro	Val	Val	Gln	Val	Phe	Ile	Ala
				125					130					135
Val	Glu	Arg	Asp	Ala	Gln	Pro	Ser	Lys	Thr	Cys	Gln	Val	Phe	Leu
				140					145					150
Ser	Cys	Trp	Ala	Pro	Asn	Ile	Ser	Glu	Ile	Thr	Tyr	Ser	Trp	Arg
				155					160					165
Arg	Glu	Thr	Thr	Met	Asp	Phe	Gly	Met	Glu	Pro	His	Ser	Leu	Phe
				170					175					180
Thr	Asp	Gly	Gln	Val	Leu	Ser	Ile	Ser	Leu	Gly	Pro	Gly	Asp	Arg
				185					190					195
Asp	Val	Ala	Tyr	Ser	Cys	Ile	Val	Ser	Asn	Pro	Val	Ser	Trp	Asp
				200					205					210
Leu	Ala	Thr	Val	Thr	Pro	Trp	Asp	Ser	Cys	His	His	Glu	Ala	Ala
				215					220					225
Pro	Gly	Lys	Ala	Ser	Tyr	Lys	Asp	Val	Leu	Leu	Val	Val	Val	Pro
				230					235					240
Val	Ser	Leu	Leu	Leu	Met	Leu	Val	Thr	Leu	Phe	Ser	Ala	Trp	His
				245					250					255
Trp	Cys	Pro	Cys	Ser	Gly	Lys	Lys	Lys	Lys	Asp	Val	His	Ala	Asp
				260					265					270
Arg	Val	Gly	Pro	Glu	Thr	Glu	Asn	Pro	Leu	Val	Gln	Asp	Leu	Pro
				275					280					285

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT16
- (B) CLONE: 1281682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10 :

Met	Pro	Phe	Thr	Arg	Pro	Leu	Lys	His	Phe	Val	Ser	Leu	Leu	His
				5					10					15
Pro	Ser	Ala	Ser	Gln	Val	His	Asn	Ala	Gly	Gln	His	Gln	Lys	Leu
				20					25					30
Lys	Thr	Leu	Glu	Lys	Ala	Cys	Gly	Leu	Ala	Leu	Gly	Glu	Gly	Arg
				35					40					45
Glu	Gln	Asn	Leu	Cys	Thr	Ser	Leu	Phe	Asn	Leu	Glu	Ile	Arg	His
				50					55					60
Pro	Arg	Asp	Ala	Ile	Ile	Phe	Cys	Val	Ser	Ile	Val	Val	Pro	Leu
				65					70					75
Ser														

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

PF-0459 US

(A) LENGTH: 147 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: BRSTNOT07  
(B) CLONE: 1298305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11 :

Met	Thr	Ala	Ser	Thr	Gly	His	Leu	Gly	Leu	Gly	Trp	Ser	Ala	Arg	
				5					10					15	
Pro	Cys	Pro	Cys	Gly	Thr	Leu	Gly	Ser	Cys	Phe	Leu	Ser	Leu	Phe	
				20					25					30	
Ala	Ala	Leu	Leu	Trp	Leu	Ala	Ala	Ala	Val	Leu	Gln	Ala	Cys	Val	
				35					40					45	
Gly	His	Ser	Asp	Glu	Gly	Cys	Gly	Ala	Ser	Gln	Cys	Arg	Arg	Ala	
				50					55					60	
Ala	Leu	Gly	Ile	Val	Pro	Ser	Pro	Val	Ser	Val	Leu	Arg	Thr	Tyr	
				65					70					75	
Pro	Gly	Leu	His	His	Gln	Asp	Pro	Val	Phe	Gly	Phe	Arg	Arg	Pro	
				80					85					90	
Ser	Met	Gly	Lys	Thr	Arg	His	Gln	Pro	Leu	Gln	Gln	Trp	Val	Pro	
				95					100					105	
Leu	Ala	Cys	Gly	His	Gln	Leu	Gly	Asp	Pro	Gly	Ser	Gly	Pro	Leu	
				110					115					120	
Leu	Ser	Pro	Val	Ser	Leu	Cys	Cys	Gly	Phe	Trp	Ala	Val	Met	Ser	
				125					130					135	
Pro	Pro	Leu	Lys	Asp	Val	Phe	Thr	Leu	Thr	Ser	Gly				
				140					145						

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 261 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: LUNGNOT12  
(B) CLONE: 1360501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12 :

Met	Glu	Leu	Leu	Gln	Val	Thr	Ile	Leu	Phe	Leu	Leu	Pro	Ser	Ile	
				5					10					15	
Cys	Ser	Ser	Asn	Ser	Thr	Gly	Val	Leu	Glu	Ala	Ala	Asn	Asn	Ser	
				20					25					30	
Leu	Val	Val	Thr	Thr	Thr	Lys	Pro	Ser	Ile	Thr	Thr	Pro	Asn	Thr	
				35					40					45	
Glu	Ser	Leu	Gln	Lys	Asn	Val	Val	Thr	Pro	Thr	Thr	Gly	Thr	Thr	
				50					55					60	
Pro	Lys	Gly	Thr	Ile	Thr	Asn	Glu	Leu	Leu	Lys	Met	Ser	Leu	Met	
				65					70					75	
Ser	Thr	Ala	Thr	Phe	Leu	Thr	Ser	Lys	Asp	Glu	Gly	Leu	Lys	Ala	
				80					85					90	

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Thr	Thr	Thr	Asp	Val	Arg	Lys	Asn	Asp	Ser	Ile	Ile	Ser	Asn	Val
				95					100					105
Thr	Val	Thr	Ser	Val	Thr	Leu	Pro	Asn	Ala	Val	Ser	Thr	Leu	Gln
				110					115					120
Ser	Ser	Lys	Pro	Lys	Thr	Glu	Thr	Gln	Ser	Ser	Ile	Lys	Thr	Thr
				125					130					135
Glu	Ile	Pro	Gly	Ser	Val	Leu	Gln	Pro	Asp	Ala	Ser	Pro	Ser	Lys
				140					145					150
Thr	Gly	Thr	Leu	Thr	Ser	Ile	Pro	Val	Thr	Ile	Pro	Glu	Asn	Thr
				155					160					165
Ser	Gln	Ser	Gln	Val	Ile	Gly	Thr	Glu	Gly	Gly	Lys	Asn	Ala	Ser
				170					175					180
Thr	Ser	Ala	Thr	Ser	Arg	Ser	Tyr	Ser	Ser	Ile	Ile	Leu	Pro	Val
				185					190					195
Val	Ile	Ala	Leu	Ile	Val	Ile	Thr	Leu	Ser	Val	Phe	Val	Leu	Val
				200					205					210
Gly	Leu	Tyr	Arg	Met	Cys	Trp	Lys	Ala	Asp	Pro	Gly	Thr	Pro	Glu
				215					220					225
Asn	Gly	Asn	Asp	Gln	Pro	Gln	Ser	Asp	Lys	Glu	Ser	Val	Lys	Leu
				230					235					240
Leu	Thr	Val	Lys	Thr	Ile	Ser	His	Glu	Ser	Gly	Glu	His	Ser	Ala
				245					250					255
Gln	Gly	Lys	Thr	Lys	Asn									
				260										

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGNOT12
- (B) CLONE: 1362406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13 :

Met	Ala	Gly	Cys	Pro	Ala	Asp	Arg	Ser	Ile	Leu	Ala	Pro	Leu	Ala
				5					10					15
Trp	Asp	Leu	Gly	Leu	Leu	Leu	Phe	Val	Gly	Gln	His	Ser	Leu	
				20					25					30
Met	Ala	Ala	Glu	Arg	Val	Lys	Ala	Trp	Thr	Ser	Arg	Tyr	Phe	Gly
				35					40					45
Val	Leu	Gln	Arg	Ser	Leu	Tyr	Val	Ala	Cys	Thr	Ala	Leu	Ala	Leu
				50					55					60
Gln	Leu	Val	Met	Arg	Tyr	Trp	Glu	Pro	Ile	Pro	Lys	Gly	Pro	Val
				65					70					75
Leu	Trp	Glu	Ala	Arg	Ala	Glu	Pro	Trp	Ala	Thr	Trp	Val	Pro	Leu
				80					85					90
Leu	Cys	Phe	Val	Leu	His	Val	Ile	Ser	Trp	Leu	Leu	Ile	Phe	Ser
				95					100					105
Ile	Leu	Leu	Val	Phe	Asp	Tyr	Ala	Glu	Leu	Met	Gly	Leu	Lys	Gln
				110					115					120
Val	Tyr	Tyr	His	Val	Leu	Gly	Leu	Gly	Glu	Pro	Leu	Ala	Leu	Lys
				125					130					135
Ser	Pro	Arg	Ala	Leu	Arg	Leu	Phe	Ser	His	Leu	Arg	His	Pro	Val

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	140		145		150
Cys Val Glu Leu	Leu Thr Val Leu Trp	Val Val Pro Thr Leu	Gly		
	155		160		165
Thr Asp Arg Leu	Leu Leu Ala Phe Leu	Leu Thr Leu Tyr Leu	Gly		
	170		175		180
Leu Ala His Gly	Leu Asp Gln Gln Asp	Leu Arg Tyr Leu Arg	Ala		
	185		190		195
Gln Leu Gln Arg	Lys Leu His Leu Leu	Ser Arg Pro Gln Asp	Gly		
	200		205		210
Glu Ala Glu					

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LATRTUT02
- (B) CLONE: 1405329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14 :

Met Gln Pro Arg Pro Arg Gly Arg Pro Pro Arg Thr Arg Gly Asp		
	5	10
Glu Ala Pro Gln Trp His Leu Pro Asp Ala Ala Ala Leu Leu Pro		15
	20	25
Val Arg Leu Pro Leu Ala Val Leu Val Arg Gly Thr Gln Arg Pro		30
	35	40
Glu Arg Arg Arg Cys Gly Arg Leu Pro Ala Gly Val Pro Gly Ala		45
	50	55
Ala Arg Ser Val Ala Arg Ser		60
	65	

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAINOT12
- (B) CLONE: 1415223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15 :

Met Leu Ala Pro Gln Arg Thr Arg Ala Pro Ser Pro Arg Ala Ala		
	5	10
Pro Arg Pro Thr Arg Ser Met Leu Pro Ala Ala Met Lys Gly Leu		15
	20	25
		30

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Gly	Leu	Ala	Leu	Leu	Ala	Val	Leu	Leu	Cys	Ser	Ala	Pro	Ala	His	
			35						40					45	
Gly	Leu	Trp	Cys	Gln	Asp	Cys	Thr	Leu	Thr	Thr	Asn	Ser	Ser	His	
			50						55					60	
Cys	Thr	Pro	Lys	Gln	Cys	Gln	Pro	Ser	Asp	Thr	Val	Cys	Ala	Ser	
			65						70					75	
Val	Arg	Ile	Thr	Asp	Pro	Ser	Ser	Ser	Arg	Lys	Asp	His	Ser	Val	
			80						85					90	
Asn	Lys	Met	Cys	Ala	Ser	Ser	Cys	Asp	Phe	Val	Lys	Arg	His	Phe	
			95						100					105	
Phe	Ser	Asp	Tyr	Leu	Met	Gly	Phe	Ile	Asn	Ser	Gly	Ile	Leu	Lys	
			110						115					120	
Val	Asp	Val	Asp	Cys	Cys	Glu	Lys	Asp	Leu	Cys	Asn	Gly	Ala	Ala	
			125						130					135	
Gly	Ala	Gly	His	Ser	Pro	Trp	Ala	Leu	Ala	Gly	Gly	Leu	Leu	Leu	
			140						145					150	
Ser	Leu	Gly	Pro	Ala	Leu	Leu	Trp	Ala	Gly	Pro					
			155						160						

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAINOT12
- (B) CLONE: 1416553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16 :

Met	Trp	Ala	Gln	Arg	Val	Leu	Thr	Leu	Trp	Gln	Gly	Leu	Ser	Trp	
				5					10					15	
Gly	Arg	Pro	Pro	Ser	Gly	Pro	Gly	Ala	Met	Ala	Pro	Arg	Gly	Gln	
				20					25					30	
Ala	Asp	Leu	Leu	Pro	Ala	Val	Ser	Thr	Pro	Phe	Leu	Ile	Thr	Val	
				35					40					45	
Trp	Ser	Pro	Ser	Phe	Gly	Cys	Ser	Leu	Arg	Cys	Val	Leu	Gly	Ser	
				50					55					60	
Ser	Glu	Pro	Glu	Ala	Ser	Phe	Trp	Lys	Pro	Ala	Val	Leu	Pro	Ala	
				65					70					75	
Pro	Val	Gln	Lys	Pro	Leu	Ser	Pro	Ala	Phe	Pro	Gln	Ala	Gly	Val	
				80					85					90	
Gly	Val	Gly	Gly	Leu	Cys	Pro	Ser	Ser	Leu	Thr	Leu	Glu	Arg	Trp	
				95					100					105	
Glu	Ala	Gly	Asn	Leu	His	Leu	Gly	Ala	Trp	Ala	Pro	Pro	Leu	Cys	
				110					115					120	
Ala	Ser	Gly	Phe	Pro	Ala	Pro	Gly	Arg	Gly	Cys	Ser	Pro	Ser	Trp	
				125					130					135	
Thr	Pro	Ala	Cys	Pro	Ser										
				140											

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: KIDNNOT09
- (B) CLONE: 1418517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17 :

Met	Glu	Asp	Glu	Glu	Val	Ala	Glu	Ser	Trp	Glu	Glu	Ala	Ala	Asp	5	10	15
Ser	Gly	Glu	Ile	Asp	Arg	Arg	Leu	Glu	Lys	Lys	Leu	Lys	Ile	Thr	20	25	30
Gln	Lys	Glu	Ser	Arg	Lys	Ser	Lys	Ser	Pro	Pro	Lys	Val	Pro	Ile	35	40	45
Val	Ile	Gln	Asp	Asp	Ser	Leu	Pro	Ala	Gly	Pro	Pro	Pro	Gln	Ile	50	55	60
Arg	Ile	Leu	Lys	Arg	Pro	Thr	Ser	Asn	Gly	Val	Val	Ser	Ser	Pro	65	70	75
Asn	Ser	Thr	Ser	Arg	Pro	Thr	Leu	Pro	Val	Lys	Ser	Leu	Ala	Gln	80	85	90
Arg	Glu	Ala	Glu	Tyr	Ala	Glu	Ala	Arg	Lys	Arg	Ile	Leu	Gly	Ser	95	100	105
Ala	Ser	Pro	Glu	Glu	Gln	Glu	Lys	Pro	Ile	Leu	Asp	Arg	Pro		110	115	120
Thr	Arg	Ile	Ser	Gln	Pro	Glu	Asp	Ser	Arg	Gln	Pro	Asn	Asn	Val	125	130	135
Ile	Arg	Gln	Pro	Leu	Gly	Pro	Asp	Gly	Ser	Gln	Gly	Phe	Lys	Gln	140	145	150
Arg	Arg																

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 742 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PANCNOT08
- (B) CLONE: 1438165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18 :

Met	Ala	Ser	Val	His	Glu	Ser	Leu	Tyr	Phe	Asn	Pro	Met	Met	Thr	5	10	15
Asn	Gly	Val	Val	His	Ala	Asn	Val	Phe	Gly	Ile	Lys	Asp	Trp	Val	20	25	30
Thr	Pro	Tyr	Lys	Ile	Ala	Val	Leu	Val	Leu	Leu	Asn	Glu	Met	Ser	35	40	45
Arg	Thr	Gly	Glu	Gly	Ala	Val	Ser	Leu	Met	Glu	Arg	Arg	Arg	Leu	50	55	60
Asn	Gln	Leu	Leu	Leu	Pro	Leu	Leu	Gln	Gly	Pro	Asp	Ile	Thr	Leu			



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				65					70					75
Ser	Lys	Leu	Tyr	Lys	Leu	Ile	Glu	Glu	Ser	Cys	Pro	Gln	Leu	Ala
				80					85					90
Asn	Ser	Val	Gln	Ile	Arg	Ile	Lys	Leu	Met	Ala	Glu	Gly	Glu	Leu
				95					100					105
Lys	Asp	Met	Glu	Gln	Phe	Phe	Asp	Asp	Leu	Ser	Asp	Ser	Phe	Ser
				110					115					120
Gly	Thr	Glu	Pro	Glu	Val	His	Lys	Thr	Ser	Val	Val	Gly	Leu	Phe
				125					130					135
Leu	Arg	His	Met	Ile	Leu	Ala	Tyr	Ser	Lys	Leu	Ser	Phe	Ser	Gln
				140					145					150
Val	Phe	Lys	Leu	Tyr	Thr	Ala	Leu	Gln	Gln	Tyr	Phe	Gln	Asn	Gly
				155					160					165
Glu	Lys	Lys	Thr	Val	Glu	Asp	Ala	Asp	Met	Glu	Leu	Thr	Ser	Arg
				170					175					180
Asp	Glu	Gly	Glu	Arg	Lys	Met	Glu	Lys	Glu	Glu	Leu	Asp	Val	Ser
				185					190					195
Val	Arg	Glu	Glu	Glu	Val	Ser	Cys	Ser	Gly	Pro	Leu	Ser	Gln	Lys
				200					205					210
Gln	Ala	Glu	Phe	Phe	Leu	Ser	Gln	Gln	Ala	Ser	Leu	Leu	Lys	Asn
				215					220					225
Asp	Glu	Thr	Lys	Ala	Leu	Thr	Pro	Ala	Ser	Leu	Gln	Lys	Glu	Leu
				230					235					240
Asn	Asn	Leu	Leu	Lys	Phe	Asn	Pro	Asp	Phe	Ala	Glu	Ala	His	Tyr
				245					250					255
Leu	Ser	Tyr	Leu	Asn	Asn	Leu	Arg	Val	Gln	Asp	Val	Phe	Ser	Ser
				260					265					270
Thr	His	Ser	Leu	Leu	His	Tyr	Phe	Asp	Arg	Leu	Ile	Leu	Thr	Gly
				275					280					285
Ala	Glu	Ser	Lys	Ser	Asn	Gly	Glu	Glu	Gly	Tyr	Gly	Arg	Ser	Leu
				290					295					300
Arg	Tyr	Ala	Ala	Leu	Asn	Leu	Ala	Ala	Leu	His	Cys	Arg	Phe	Gly
				305					310					315
His	Tyr	Gln	Gln	Ala	Glu	Leu	Ala	Leu	Gln	Glu	Ala	Ile	Arg	Ile
				320					325					330
Ala	Gln	Glu	Ser	Asn	Asp	His	Val	Cys	Leu	Gln	His	Cys	Leu	Ser
				335					340					345
Trp	Leu	Tyr	Val	Leu	Gly	Gln	Lys	Arg	Ser	Asp	Ser	Tyr	Val	Leu
				350					355					360
Leu	Glu	His	Ser	Val	Lys	Lys	Ala	Val	His	Phe	Gly	Leu	Pro	Arg
				365					370					375
Ala	Phe	Ala	Gly	Lys	Thr	Ala	Asn	Lys	Leu	Met	Asp	Ala	Leu	Lys
				380					385					390
Asp	Ser	Asp	Leu	Leu	His	Trp	Lys	His	Ser	Leu	Ser	Glu	Leu	Ile
				395					400					405
Asp	Ile	Ser	Ile	Ala	Gln	Lys	Thr	Ala	Ile	Trp	Arg	Leu	Tyr	Gly
				410					415					420
Arg	Ser	Thr	Met	Ala	Leu	Gln	Gln	Ala	Gln	Met	Leu	Leu	Ser	Met
				425					430					435
Asn	Ser	Leu	Glu	Ala	Val	Asn	Ala	Gly	Val	Gln	Gln	Asn	Asn	Thr
				440					445					450
Glu	Ser	Phe	Ala	Val	Ala	Leu	Cys	His	Leu	Ala	Glu	Leu	His	Ala
				455					460					465
Glu	Gln	Gly	Cys	Phe	Ala	Ala	Ala	Ser	Glu	Val	Leu	Lys	His	Leu
				470					475					480
Lys	Glu	Arg	Phe	Pro	Pro	Asn	Ser	Gln	His	Ala	Gln	Leu	Trp	Met
				485					490					495
Leu	Cys	Asp	Gln	Lys	Ile	Gln	Phe	Asp	Arg	Ala	Met	Asn	Asp	Gly
				500					505					510
Lys	Tyr	His	Leu	Ala	Asp	Ser	Leu	Val	Thr	Gly	Ile	Thr	Ala	Leu
				515					520					525

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Asn	Ser	Ile	Glu	Gly	Val	Tyr	Arg	Lys	Ala	Val	Val	Leu	Gln	Ala	
				530					535					540	
Gln	Asn	Gln	Met	Ser	Glu	Ala	His	Lys	Leu	Leu	Gln	Lys	Leu	Leu	
				545					550					555	
Val	His	Cys	Gln	Lys	Leu	Lys	Asn	Thr	Glu	Met	Val	Ile	Ser	Val	
				560					565					570	
Leu	Leu	Ser	Val	Ala	Glu	Leu	Tyr	Trp	Arg	Ser	Ser	Ser	Pro	Thr	
				575					580					585	
Ile	Ala	Leu	Pro	Met	Leu	Leu	Gln	Ala	Leu	Ala	Leu	Ser	Lys	Glu	
				590					595					600	
Tyr	Arg	Leu	Gln	Tyr	Leu	Ala	Ser	Glu	Thr	Val	Leu	Asn	Leu	Ala	
				605					610					615	
Phe	Ala	Gln	Leu	Ile	Leu	Gly	Ile	Pro	Glu	Gln	Ala	Leu	Ser	Leu	
				620					625					630	
Leu	His	Met	Ala	Ile	Glu	Pro	Ile	Leu	Ala	Asp	Gly	Ala	Ile	Leu	
				635					640					645	
Asp	Lys	Gly	Arg	Ala	Met	Phe	Leu	Val	Ala	Lys	Cys	Gln	Val	Ala	
				650					655					660	
Ser	Ala	Ala	Ser	Tyr	Asp	Gln	Pro	Lys	Lys	Ala	Glu	Ala	Leu	Glu	
				665					670					675	
Ala	Ala	Ile	Glu	Asn	Leu	Asn	Glu	Ala	Lys	Asn	Tyr	Phe	Ala	Lys	
				680					685					690	
Val	Asp	Cys	Lys	Glu	Arg	Ile	Arg	Asp	Val	Val	Tyr	Phe	Gln	Ala	
				695					700					705	
Arg	Leu	Tyr	His	Thr	Leu	Gly	Lys	Thr	Gln	Glu	Arg	Asn	Arg	Cys	
				710					715					720	
Ala	Met	Leu	Phe	Arg	Gln	Leu	His	Gln	Glu	Leu	Pro	Ser	His	Gly	
				725					730					735	
Val	Pro	Leu	Ile	Asn	His	Leu									
				740											

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THYRN0T03
- (B) CLONE: 1440381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19 :

Met	Asp	Gly	Ile	Leu	Asp	Glu	Ser	Leu	Leu	Glu	Thr	Cys	Pro	Ile	
				5					10					15	
Gln	Ser	Pro	Leu	Gln	Val	Phe	Ala	Gly	Met	Gly	Gly	Leu	Ala	Leu	
				20					25					30	
Ile	Ala	Glu	Arg	Leu	Pro	Met	Leu	Tyr	Pro	Glu	Val	Ile	Gln	Gln	
				35					40					45	
Val	Ser	Ala	Pro	Val	Val	Thr	Ser	Thr	Thr	Gln	Glu	Lys	Pro	Tyr	
				50					55					60	
Asp	Ser	Asp	Gln	Phe	Glu	Trp	Val	Thr	Ile	Glu	Gln	Ser	Gly	Glu	
				65					70					75	
Leu	Val	Tyr	Glu	Ala	Pro	Glu	Thr	Val	Ala	Ala	Glu	Pro	Pro	Pro	
				80					85					90	
Ile	Lys	Ser	Ala	Val	Gln	Thr	Met	Ser	Pro	Ile	Pro	Ala	His	Ser	

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Leu	Ala	Ala	Phe	95	Leu	Phe	Leu	Arg	100	Leu	Pro	Gly	Tyr	Ala	105	Glu
				110					115							120
Val	Leu	Leu	Lys	125	Arg	Lys	His	Ala	130	Gln	Cys	Leu	Leu	Arg	135	Leu
Val	Leu	Gly	Val	140	Thr	Asp	Asp	Gly	145	Gly	Ser	His	Ile	Leu	150	Gln
Ser	Pro	Ser	Ala	155	Asn	Val	Leu	Pro	160	Leu	Pro	Phe	His	Val	165	Leu
Arg	Ser	Leu	Phe	170	Ser	Thr	Thr	Pro	175	Leu	Thr	Asp	Asp	Gly	180	Val
Leu	Leu	Arg	Arg	185	Met	Ala	Leu	Glu	190	Gly	Ala	Leu	His	Leu	195	Ile
Leu	Val	Cys	Leu	200	Ser	Ala	Leu	Ser	205	His	Ser	Pro	Arg	Val	210	Pro
Asn	Ser	Ser	Val	215	Asn	Gln	Thr	Glu	220	Gln	Val	Ser	Ser	Ser	225	His
Asn	Pro	Thr	Ser	230	Thr	Glu	Glu	Gln	235	Leu	Tyr	Trp	Ala	Lys	240	Gly
Thr	Gly	Phe	Gly	245	Thr	Gly	Ser	Thr	250	Ser	Gly	Trp	Asp	Val	255	Glu
Gln	Ala	Leu	Thr	260	Lys	Gln	Arg	Leu	265	Glu	Glu	His	Val	Thr	270	Cys
Leu	Leu	Gln	Val	275	Leu	Ala	Ser	Tyr	280	Asn	Pro	Val	Ser	Ser	285	Ala
Val	Asn	Gly	Glu	290	Ala	Gln	Ser	Ser	295	Glu	Thr	Arg	Gly	Gln	300	Asn
Ser	Asn	Ala	Leu	305	Pro	Ser	Val	Leu	310	Glu	Leu	Leu	Ser	Gln	315	Ser
Cys	Leu	Ile	Pro	320	Ala	Met	Ser	Ser	325	Leu	Arg	Asn	Asp	Ser	330	Val
Leu	Asp	Met	Ala	335	Arg	His	Val	Pro	340	Leu	Tyr	Arg	Ala	Leu	345	Glu
Leu	Leu	Arg	Ala	350	Ile	Ala	Ser	Cys	355	Ala	Met	Val	Pro	Leu	360	Leu
Leu	Pro	Leu	Ser	365	Thr	Glu	Asn	Gly	370	Glu	Glu	Glu	Glu	Gln	375	Ser
Glu	Cys	Gln	Thr	380	Ser	Val	Gly	Thr	385	Leu	Leu	Ala	Lys	Met	390	Thr
Cys	Val	Asp	Thr	395	Tyr	Thr	Asn	Arg	400	Arg	Ser	Lys	Arg	Glu	405	Asn
Val	Lys	Thr	Gly	410	Val	Lys	Pro	Asp	415	Ser	Asp	Gln	Glu	Pro	420	Glu
Gly	Leu	Thr	Leu	425	Leu	Val	Pro	Asp	430	Gln	Lys	Thr	Ala	Glu	435	Ile
Val	Tyr	Ala	Ala	440	Thr	Thr	Ser	Leu	445	Gln	Ala	Asn	Gln	Glu	450	Lys
Asn	Trp	Val	Asn	455	Thr	Pro	Arg	Arg	460	Leu	Met	Asn	Pro	Lys	465	Pro
Leu	Ser	Val	Leu	470	Lys	Ser	Leu	Glu	475	Glu	Lys	Tyr	Val	Ala	480	Met
Lys	Lys	Leu	Gln	485	Phe	Asp	Thr	Phe	490	Met	Val	Ser	Glu	Asp	495	Glu
Asp	Gly	Lys	Leu	500	Gly	Phe	Lys	Val	505	Tyr	His	Tyr	Met	Ser	510	Gln
Val	Lys	Asn	Ala	515	Asn	Asp	Ala	Asn	520	Ala	Ala	Arg	Ala	Arg	525	Arg
Leu	Ala	Gln	Glu	530	Ala	Val	Thr	Leu	535	Thr	Ser	Leu	Pro	Leu	540	Ser
Ser	Ser	Ser	Ser	545	Val	Phe	Val	Arg	550	Asp	Glu	Glu	Arg	Leu	555	Asp

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Ile	Met	Lys	Val	Leu	Ile	Thr	Gly	Pro	Ala	Asp	Thr	Pro	Tyr	Ala	
				560					565					570	
Asn	Gly	Cys	Phe	Glu	Phe	Asp	Val	Tyr	Phe	Pro	Gln	Asp	Tyr	Pro	
				575					580					585	
Ser	Ser	Pro	Pro	Leu	Val	Asn	Leu	Glu	Thr	Thr	Gly	Gly	His	Ser	
				590					595					600	
Val	Arg	Phe	Asn	Pro	Asn	Leu	Tyr	Asn	Asp	Gly	Lys	Val	Cys	Leu	
				605					610					615	
Ser	Ile	Leu	Asn	Thr	Trp	His	Gly	Arg	Pro	Glu	Glu	Lys	Trp	Asn	
				620					625					630	
Pro	Gln	Thr	Ser	Ser	Phe	Leu	Gln	Val	Leu	Val	Ser	Val	Gln	Ser	
				635					640					645	
Leu	Ile	Leu	Val	Ala	Glu	Pro	Tyr	Phe	Asn	Glu	Pro	Gly	Tyr	Glu	
				650					655					660	
Arg	Ser	Arg	Gly	Thr	Pro	Ser	Gly	Thr	Gln	Ser	Ser	Arg	Glu	Tyr	
				665					670					675	
Asp	Gly	Asn	Ile	Arg	Gln	Ala	Thr	Val	Lys	Trp	Ala	Met	Leu	Glu	
				680					685					690	
Gln	Ile	Arg	Asn	Pro	Ser	Pro	Cys	Phe	Lys	Glu	Val	Ile	His	Lys	
				695					700					705	
His	Phe	Tyr	Leu	Lys	Arg	Val	Glu	Ile	Met	Ala	Gln	Cys	Glu	Glu	
				710					715					720	
Trp	Ile	Ala	Asp	Ile	Gln	Gln	Tyr	Ser	Ser	Asp	Lys	Arg	Val	Gly	
				725					730					735	
Arg	Thr	Met	Ser	His	His	Ala	Ala	Ala	Leu	Lys	Arg	His	Thr	Ala	
				740					745					750	
Gln	Leu	Arg	Glu	Glu	Leu	Leu	Lys	Leu	Pro	Cys	Pro	Glu	Gly	Leu	
				755					760					765	
Asp	Pro	Asp	Thr	Asp	Asp	Ala	Pro	Glu	Val	Cys	Arg	Ala	Thr	Thr	
				770					775					780	
Gly	Ala	Glu	Glu	Thr	Leu	Met	His	Asp	Gln	Val	Lys	Pro	Ser	Ser	
				785					790					795	
Ser	Lys	Glu	Leu	Pro	Ser	Asp	Phe	Gln	Leu						
				800					805						

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGNOT14
- (B) CLONE: 1510839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20 :

Met	Lys	Ala	Ser	Gln	Cys	Cys	Cys	Cys	Leu	Ser	His	Leu	Leu	Ala	
				5					10					15	
Ser	Val	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Glu	Leu	Ser	Gly	Pro	Leu	
				20					25					30	
Ala	Val	Leu	Leu	Gln	Ala	Ala	Glu	Ala	Ala	Pro	Gly	Leu	Gly	Pro	
				35					40					45	
Pro	Asp	Pro	Arg	Pro	Arg	Thr	Leu	Pro	Pro	Leu	Pro	Pro	Gly	Pro	
				50					55					60	
Thr	Pro	Ala	Gln	Gln	Pro	Gly	Arg	Gly	Leu	Ala	Glu	Ala	Ala	Gly	

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Pro	Arg	Gly	Ser	65	Gly	Gly	Asn	Gly	70	Ser	Asn	Pro	Val	Ala	Gly	75
				80					85							90
Leu	Glu	Thr	Asp	95	His	Gly	Gly	Lys	100	Ala	Gly	Glu	Gly	Ser	Val	105
				110					115							120
Gly	Gly	Gly	Leu	125	Ala	Val	Ser	Pro	130	Pro	Gly	Asp	Lys	Pro	Met	135
				140					145							150
Thr	Gln	Arg	Ala	155	Leu	Thr	Val	Leu	160	Val	Val	Ser	Gly	Ala	Val	165
				170					175							180
Leu	Val	Tyr	Phe	185	Val	Val	Arg	Thr	190	Arg	Met	Arg	Arg	Arg	Asn	195
Arg	Lys	Thr	Arg		Arg	Tyr	Gly	Val		Asp	Thr	Asn	Ile	Glu	Asn	
Met	Glu	Leu	Thr		Pro	Leu	Glu	Gln		Asp	Glu	Asp	Asp	Asp	Asn	
Thr	Leu	Phe	Asp		Ala	Asn	His	Pro		Arg	Arg	Glu	Cys	Ala	Phe	

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SPLNNOT04
- (B) CLONE: 1534876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21 :

Met	Trp	Phe	Leu	Gly	Cys	Thr	Gly	Pro	Gly	Cys	Gly	Cys	Ala	Gly		
				5					10					15		
Val	Cys	Lys	Val	20	Pro	Cys	Ile	Ser	25	Thr	Gly	Phe	Glu	Thr	Ser	
				35					40							
Gly	Pro	Cys	Pro	50	Ser	Arg	Glu	Gly	55	Phe	Leu	Phe	Phe	Leu	Thr	
				65					70							
Gln	Val	Thr	Phe	80	Gln	Pro	Phe	Gln	85	Pro	Ser	Phe	Ser	Ala	Leu	
				95					100							
Pro	Ser	Asn	Ser	110	Ala	Asn	Pro	Gly	115	Val	Gly	Ser	Gln	Gly	Gly	Arg
				125					130							
Glu	Cys	Pro	Thr	140	Thr	Phe	Ser	Gly	145	Gln	Pro	Leu	Thr	Pro	Lys	Pro
				155					160							
Leu	Pro	Pro	Ser		Ile	Leu	His	Pro		Leu	Pro	Ile	Gln	Pro	Lys	Cys
Pro	Gln	Leu	Gly		Leu	Ser	Cys	Ile		Pro	Val	Glu	Gly	Pro	Leu	Pro
Cys	Leu	Ser	Glu		Val	Arg	Leu	Cys		Cys	Val	Met	Gly	Arg	Leu	Cys
Pro	Ser	Pro	Pro		Leu	Ala	Arg	Cys		Thr	Cys	Phe	Leu	Val	Cys	Thr
Arg	Cys	Pro	Gly		Pro	Ser	Leu	Pro		Cys	Gln					

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SPLNNOT04
- (B) CLONE: 1559131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22 :

Met	Asp	Lys	Leu	Lys	Lys	Val	Leu	Ser	Gly	Gln	Asp	Thr	Glu	Asp	5	10	15
Arg	Ser	Gly	Leu	Ser	Glu	Val	Val	Glu	Ala	Ser	Ser	Leu	Ser	Trp	20	25	30
Ser	Thr	Arg	Ile	Lys	Gly	Phe	Ile	Ala	Cys	Phe	Ala	Ile	Gly	Ile	35	40	45
Leu	Cys	Ser	Leu	Leu	Gly	Thr	Val	Leu	Leu	Trp	Val	Pro	Arg	Lys	50	55	60
Gly	Leu	His	Leu	Phe	Ala	Val	Phe	Tyr	Thr	Phe	Gly	Asn	Ile	Ala	65	70	75
Ser	Ile	Gly	Ser	Thr	Ile	Phe	Leu	Met	Gly	Pro	Val	Lys	Gln	Leu	80	85	90
Lys	Arg	Met	Phe	Glu	Pro	Thr	Arg	Leu	Ile	Ala	Thr	Ile	Met	Val	95	100	105
Leu	Leu	Cys	Phe	Ala	Leu	Thr	Leu	Cys	Ser	Ala	Phe	Trp	Trp	His	110	115	120
Asn	Lys	Gly	Leu	Ala	Leu	Ile	Phe	Cys	Ile	Leu	Gln	Ser	Leu	Ala	125	130	135
Leu	Thr	Trp	Tyr	Ser	Leu	Ser	Phe	Ile	Pro	Phe	Ala	Arg	Asp	Ala	140	145	150
Val	Lys	Lys	Cys	Phe	Ala	Val	Cys	Leu	Ala						155	160	

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADNOT03
- (B) CLONE: 1601473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23 :

Met	Gln	Ala	Lys	Tyr	Ser	Ser	Thr	Arg	Asp	Met	Leu	Asp	Asp	Asp	5	10	15
Gly	Asp	Thr	Thr	Met	Ser	Leu	His	Ser	Gln	Ala	Ser	Ala	Thr	Thr	20	25	30
Arg	His	Pro	Glu	Pro	Arg	Arg	Thr	Glu	His	Arg	Ala	Pro	Ser	Ser	35	40	45
Thr	Trp	Arg	Pro	Val	Ala	Leu	Thr	Leu	Leu	Thr	Leu	Cys	Leu	Val	50	55	60

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Leu Leu Ile Gly Leu Ala Ala Leu Gly Leu Leu Cys Lys Ser Ala  
65 70 75  
Leu

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BRAITUT12

(B) CLONE: 1615809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24 :

Met Ile Ser Tyr Ile Val Leu Leu Ser Ile Leu Leu Trp Pro Leu  
5 10 15  
Val Val Tyr His Glu Leu Ile Gln Arg Met Tyr Thr Arg Leu Glu  
20 25 30  
Pro Leu Leu Met Gln Leu Asp Tyr Ser Met Lys Ala Glu Ala Asn  
35 40 45  
Ala Leu His His Lys His Asp Lys Arg Lys Arg Gln Gly Lys Asn  
50 55 60  
Ala Pro Pro Gly Gly Asp Glu Pro Leu Ala Glu Thr Glu Ser Glu  
65 70 75  
Ser Glu Ala Glu Leu Ala Gly Phe Ser Pro Val Val Asp Val Lys  
80 85 90  
Lys Thr Ala Leu Ala Leu Ala Ile Thr Asp Ser Glu Leu Ser Asp  
95 100 105  
Glu Glu Ala Ser Ile Leu Glu Ser Gly Gly Phe Ser Val Ser Arg  
110 115 120  
Ala Thr Thr Pro Gln Leu Thr Asp Val Ser Glu Asp Leu Asp Gln  
125 130 135  
Gln Ser Leu Pro Ser Glu Pro Glu Glu Thr Leu Ser Arg Asp Leu  
140 145 150  
Gly Glu Gly Glu Glu Gly Glu Leu Ala Pro Pro Glu Asp Leu Leu  
155 160 165  
Gly Arg Pro Gln Ala Leu Ser Arg Gln Ala Leu Asp Ser Glu Glu  
170 175 180  
Glu Glu Glu Asp Val Ala Ala Lys Glu Thr Leu Leu Arg Leu Ser  
185 190 195  
Ser Pro Leu His Phe Val Asn Thr His Phe Asn Gly Ala Gly Ser  
200 205 210  
Pro Gln Asp Gly Val Lys Cys Ser Pro Gly Gly Pro Val Glu Thr  
215 220 225  
Leu Ser Pro Glu Thr Val Ser Gly Gly Leu Thr Ala Leu Pro Gly  
230 235 240  
Thr Leu Ser Pro Pro Leu Cys Leu Val Gly Ser Asp Pro Ala Pro  
245 250 255  
Ser Pro Ser Ile Leu Pro Pro Val Pro Gln Asp Ser Pro Gln Pro  
260 265 270  
Leu Pro Ala Pro Glu Glu Glu Glu Ala Leu Thr Thr Glu Asp Phe  
275 280 285  
Glu Leu Leu Asp Gln Gly Glu Leu Glu Gln Leu Asn Ala Glu Leu  
290 295 300  
Gly Leu Glu Pro Glu Thr Pro Pro Lys Pro Pro Asp Ala Pro Pro  
305 310 315  
Leu Gly Pro Asp Ile His Ser Leu Val Gln Ser Asp Gln Glu Ala

Gln Ala Val Ala Glu Pro  
320  
335

325

330

## (2) INFORMATION FOR SEQ ID NO: 25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT19
- (B) CLONE: 1634813

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25 :

Met	Asn	Leu	Trp	Leu	Leu	Ala	Cys	Leu	Val	Ala	Gly	Phe	Leu	Gly	5	10	15
Ala	Trp	Ala	Pro	Ala	Val	His	Ala	Gln	Gly	Val	Phe	Glu	Asp	Cys	20	25	30
Cys	Leu	Ala	Tyr	His	Tyr	Pro	Ile	Gly	Trp	Ala	Val	Leu	Arg	Arg	35	40	45
Ala	Trp	Thr	Tyr	Arg	Ile	Gln	Glu	Val	Ser	Gly	Ser	Cys	Asn	Leu	50	55	60
Pro	Ala	Ala	Ile	Phe	Tyr	Leu	Pro	Lys	Arg	His	Arg	Lys	Val	Cys	65	70	75
Gly	Asn	Pro	Lys	Ser	Arg	Glu	Val	Gln	Arg	Ala	Met	Lys	Leu	Leu	80	85	90
Asp	Ala	Arg	Asn	Lys	Val	Phe	Ala	Lys	Leu	Arg	His	Asn	Thr	Gln	95	100	105
Thr	Phe	Gln	Ala	Gly	Pro	His	Ala	Val	Lys	Lys	Leu	Ser	Ser	Gly	110	115	120
Asn	Ser	Lys	Leu	Ser	Ser	Ser	Lys	Phe	Ser	Asn	Pro	Ile	Ser	Ser	125	130	135
Ser	Lys	Arg	Asn	Val	Ser	Leu	Leu	Ile	Ser	Ala	Asn	Ser	Gly	Leu	140	145	150

## (2) INFORMATION FOR SEQ ID NO: 26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UTRSNOT06
- (B) CLONE: 1638407

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26 :

Met	Ala	Pro	Pro	Ala	Leu	Gln	Arg	Gly	Gln	Arg	Val	Ala	Ala	Val	5	10	15
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---	----	----



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Ala	Val	Gly	Ser	Gln	Ala	Val	Leu	Gln	Ile	Leu	Ser	Arg	Val	Ser	
				20					25					30	
Gly	Arg	Gln	Ala	Pro	Gln	Pro	Ser	Gly	Ser	Gly	Gly	Val	Gly		
				35				40						45	
Ala	Gly	Pro	Val	Val	Val	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Pro	Gln	
				50				55						60	
Pro	His	Pro	Ser	Ser	Ser	Gln	Ser	Pro	Pro	Asp	Leu	Pro	Leu	Lys	
				65				70						75	
Ala	Gly	Asp	Thr	Val	Met	Gly	Lys	Gln	Ala	Gln	Arg	Asp	Ile	Arg	
				80				85						90	
Leu	Arg	Val	Arg	Ala	Glu	Tyr	Cys	Glu	His	Gly	Pro	Ala	Leu	Glu	
				95				100						105	
Gln	Gly	Val	Ala	Ser	Arg	Arg	Pro	Gln	Ala	Leu	Ala	Arg	Gln	Leu	
				110				115						120	
Asp	Val	Phe	Gly	Gln	Ala	Thr	Ala	Val	Leu	Arg	Ser	Arg	Asp	Leu	
				125				130						135	
Gly	Ser	Val	Val	Cys	Asp	Ile	Lys	Phe	Ser	Glu	Leu	Ser	Tyr	Leu	
				140				145						150	
Asp	Ala	Phe	Trp	Gly	Asp	Tyr	Leu	Ser	Gly	Ala	Leu	Leu	Gln	Ala	
				155				160						165	
Leu	Arg	Gly	Val	Phe	Leu	Thr	Glu	Ala	Leu	Arg	Glu	Ala	Val	Gly	
				170				175						180	
Arg	Glu	Ala	Val	Arg	Leu	Leu	Val	Ser	Val	Asp	Glu	Ala	Asp	Tyr	
				185				190						195	
Glu	Ala	Gly	Arg	Arg	Arg	Leu	Leu	Leu	Met	Ala	Glu	Glu	Gly	Gly	
				200				205						210	
Arg	Arg	Pro	Thr	Glu	Ala	Ser									
				215											

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSTUT08
- (B) CLONE: 1653112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27 :

Met	Ser	Gln	Pro	Arg	Thr	Pro	Glu	Gln	Ala	Leu	Asp	Thr	Pro	Gly	
				5					10					15	
Asp	Cys	Pro	Pro	Gly	Arg	Arg	Asp	Glu	Asp	Ala	Gly	Glu	Gly	Ile	
				20				25						30	
Gln	Cys	Ser	Gln	Arg	Met	Leu	Ser	Phe	Ser	Asp	Ala	Leu	Leu	Ser	
				35				40						45	
Ile	Ile	Ala	Thr	Val	Met	Ile	Leu	Pro	Val	Thr	His	Thr	Glu	Ile	
				50				55						60	
Ser	Pro	Glu	Gln	Gln	Phe	Asp	Arg	Ser	Val	Gln	Arg	Leu	Leu	Ala	
				65				70						75	
Thr	Arg	Ile	Ala	Val	Tyr	Leu	Met	Thr	Phe	Leu	Ile	Val	Thr	Val	
				80				85						90	
Ala	Trp	Ala	Ala	His	Thr	Arg	Leu	Phe	Gln	Val	Val	Gly	Lys	Thr	
				95				100						105	
Asp	Asp	Thr	Leu	Ala	Leu	Leu	Asn	Leu	Ala	Cys	Met	Met	Thr	Ile	

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Thr Phe Leu Pro	110	Thr Phe Ser Leu	115	Val Thr Phe Pro	120
Tyr	125	Met	130	Val Thr Phe Pro	135
Val Pro Leu Gly	140	Ile Phe Leu Phe Cys	145	Val Cys Val Ile Ala	150
Gly Val Val Gln	155	Ala Leu Ile Val Gly	160	Tyr Ala Phe His Phe	165
His Leu Leu Ser	170	Pro Gln Ile Gln Arg	175	Ser Ala His Arg Ala	180
Tyr Arg Arg His	185	Val Leu Gly Ile Val	190	Leu Gln Gly Pro Ala	195
Cys Phe Ala Ala	200	Ala Ile Phe Ser Leu	205	Phe Phe Val Pro Leu	210
Tyr Leu Leu Met	215	Val Thr Val Ile Leu	220	Leu Pro Tyr Val Ser	225
Val Thr Gly Trp	230	Cys Arg Asp Arg Leu	235	Leu Gly His Arg Glu	240
Ser Ala His Pro	245	Val Glu Val Phe Ser	250	Phe Asp Leu His Glu	255
Leu Ser Lys Glu	260	Arg Val Glu Ala Phe	265	Ser Asp Gly Val Tyr	270
Ile Val Ala Thr	275	Leu Leu Ile Leu Asp	280	Ile Cys Glu Asp Asn	285
Pro Asp Pro Lys	290	Asp Val Lys Glu Arg	295	Phe Ser Gly Ser Leu	300
Ala Ala Leu Ser	305	Ala Thr Gly Pro Arg	310	Phe Leu Ala Tyr Phe	315
Ser Phe Ala Thr	320	Val Gly Leu Leu Trp	325	Phe Ala His His Ser	330
Phe Leu His Val	335	Arg Lys Ala Thr Arg	340	Ala Met Gly Leu Leu	345
Thr Leu Ser Leu	350	Ala Phe Val Gly Gly	355	Leu Pro Leu Ala Tyr	360
Gln Thr Ser Ala	365	Phe Ala Arg Gln Pro	370	Arg Asp Glu Leu Glu	375
Val Arg Val Ser	380	Cys Thr Ile Ile Phe	385	Leu Ala Ser Ile Phe	390
Leu Ala Met Trp	395	Thr Thr Ala Leu Leu	400	His Gln Ala Glu Thr	405
Gln Pro Ser Val	410	Trp Phe Gly Gly Arg	415	Glu His Val Leu Met	420
Ala Lys Leu Ala	425	Leu Tyr Pro Cys Ala	430	Ser Leu Leu Ala Phe	435
Ser Thr Cys Leu	440	Leu Ser Arg Phe Ser	445	Val Gly Ile Phe His	450
Met Gln Ile Ala	455	Val Pro Cys Ala Phe	460	Leu Leu Leu Arg Leu	465
Val Gly Leu Ala	470	Leu Ala Thr Leu Arg	475	Val Leu Arg Gly Leu	480
Arg Pro Glu His	485	Pro Pro Pro Ala Pro	490	Thr Gly Gln Asp Asp	495
Gln Ser Gln Leu	500	Leu Pro Ala Pro Cys			

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 320 amino acids

PF-0459 US

(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: BRSTNOT09  
(B) CLONE: 1664634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28 :

Met	Ala	Ala	Arg	Leu	Asp	Gly	Gly	Phe	Ala	Ala	Val	Ser	Arg	Ala	
				5					10					15	
Phe	His	Glu	Ile	Arg	Ala	Arg	Asn	Pro	Ala	Phe	Gln	Pro	Gln	Thr	
				20					25					30	
Leu	Met	Asp	Phe	Gly	Ser	Gly	Thr	Gly	Ser	Val	Thr	Trp	Ala	Ala	
				35					40					45	
His	Ser	Ile	Trp	Gly	Gln	Ser	Leu	Arg	Glu	Tyr	Met	Cys	Val	Asp	
				50					55					60	
Arg	Ser	Ala	Ala	Met	Leu	Val	Leu	Ala	Glu	Lys	Leu	Leu	Thr	Gly	
				65					70					75	
Gly	Ser	Glu	Ser	Gly	Glu	Pro	Tyr	Ile	Pro	Gly	Val	Phe	Phe	Arg	
				80					85					90	
Gln	Phe	Leu	Pro	Val	Ser	Pro	Lys	Val	Gln	Phe	Asp	Val	Val	Val	
				95					100					105	
Ser	Ala	Phe	Ser	Leu	Ser	Asp	Gln	Leu	Leu	Thr	Phe	Ile	Leu	Ser	
				110					115					120	
Cys	Asn	Ser	Ser	Leu	Leu	His	Ile	Phe	Pro	Phe	Cys	Glu	Gln	Val	
				125					130					135	
Leu	Val	Glu	Asn	Gly	Thr	Lys	Ala	Gly	His	Ser	Leu	Leu	Met	Asp	
				140					145					150	
Ala	Arg	Asp	Leu	Val	Leu	Lys	Gly	Lys	Glu	Lys	Ser	Pro	Leu	Asp	
				155					160					165	
Pro	Arg	Pro	Gly	Phe	Val	Phe	Ala	Pro	Cys	Pro	His	Glu	Leu	Pro	
				170					175					180	
Cys	Pro	Gln	Leu	Thr	Asn	Leu	Ala	Cys	Ser	Phe	Ser	Gln	Ala	Tyr	
				185					190					195	
His	Pro	Ile	Pro	Phe	Ser	Trp	Asn	Lys	Lys	Pro	Lys	Glu	Glu	Lys	
				200					205					210	
Phe	Ser	Met	Val	Ile	Leu	Ala	Arg	Gly	Ser	Pro	Glu	Glu	Ala	His	
				215					220					225	
Arg	Trp	Pro	Arg	Ile	Thr	Gln	Pro	Val	Leu	Lys	Arg	Pro	Arg	His	
				230					235					240	
Val	His	Cys	His	Leu	Cys	Cys	Pro	Asp	Gly	His	Met	Gln	His	Ala	
				245					250					255	
Val	Leu	Thr	Ala	Arg	Arg	His	Gly	Arg	Tyr	Gly	Gly	Cys	Asp	Gln	
				260					265					270	
Asn	Gln	Trp	Asp	Val	Ala	Gly	Ser	Cys	Ser	Pro	Arg	Gln	His	Leu	
				275					280					285	
Phe	Pro	Gln	Gly	Phe	Val	Ser	Leu	Cys	Pro	Cys	Gln	Leu	Leu	Gly	
				290					295					300	
Arg	Ser	Phe	Thr	Cys	Ala	Tyr	Ser	Val	Cys	Val	Ser	Ser	Ile	Tyr	
				305					310					315	
Gly	Ser	Gly	Ser	Leu											
				320											

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

PF-0459 US

(A) LENGTH: 117 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: PROSTUT10  
(B) CLONE: 1690990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29 :

Met	Asp	Asn	Lys	Gly	Ile	Tyr	Pro	Gly	Ala	Val	Phe	Tyr	His	Asp	
				5					10					15	
Ser	Phe	Thr	Glu	Ser	Arg	Val	Val	Leu	Leu	Arg	Ile	Arg	Thr	Leu	
				20					25					30	
Val	Pro	Tyr	Ser	Pro	Pro	Asp	Cys	Pro	Thr	Thr	Thr	Thr	Ala	Tyr	
				35					40					45	
Ser	Pro	Phe	Pro	Asn	His	Gly	Gln	Gln	Ile	Glu	Leu	Leu	Thr	Glu	
				50					55					60	
Val	Ser	Phe	Arg	Trp	Ile	Ser	Gln	Pro	Phe	Pro	His	Arg	Pro	His	
				65					70					75	
Arg	Glu	Thr	Val	Thr	Asp	Cys	Tyr	Ser	Pro	Asn	Thr	Gln	Val	Lys	
				80					85					90	
Ser	Asn	Ala	Gly	Arg	Asn	Asn	Ser	Lys	Ser	Phe	Asn	Phe	Leu	Ile	
				95					100					105	
Leu	Leu	Leu	Lys	Ile	Leu	Thr	Glu	Ala	Ser	Arg	Phe				
				110					115						

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 298 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: DUODNOT02  
(B) CLONE: 1704050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30 :

Met	Ala	Arg	Arg	Ser	Arg	His	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Arg	
				5					10					15	
Tyr	Leu	Val	Val	Ala	Leu	Gly	Tyr	His	Lys	Ala	Tyr	Gly	Phe	Ser	
				20					25					30	
Ala	Pro	Lys	Asp	Gln	Gln	Val	Val	Thr	Ala	Val	Glu	Tyr	Gln	Glu	
				35					40					45	
Ala	Ile	Leu	Ala	Cys	Lys	Thr	Pro	Lys	Lys	Thr	Val	Ser	Ser	Arg	
				50					55					60	
Leu	Glu	Trp	Lys	Lys	Leu	Gly	Arg	Ser	Val	Ser	Phe	Val	Tyr	Tyr	
				65					70					75	
Gln	Gln	Thr	Leu	Gln	Gly	Asp	Phe	Lys	Asn	Arg	Ala	Glu	Met	Ile	
				80					85					90	
Asp	Phe	Asn	Ile	Arg	Ile	Lys	Asn	Val	Thr	Arg	Ser	Asp	Ala	Gly	
				95					100					105	
Lys	Tyr	Arg	Cys	Glu	Val	Ser	Ala	Pro	Ser	Glu	Gln	Gly	Gln	Asn	
				110					115					120	

**SECRET**

(2) INFORMATION FOR SEQ ID NO: 31:

(A) LENGTH: 118 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(A) LIBRARY: PROSNOT16  
(B) CLONE: 1711840

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(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32 :

Met	Gln	Thr	Cys	5	Leu	Ala	Phe	Pro	Gly	10	His	Val	Ser	Gln	Ala	15
Leu	Gly	Thr	Leu	20	Phe	Leu	Ala	Ala	Ser	25	Leu	Ser	Ala	Gln	Asn	30
Glu	Gly	Trp	Asp	35	Pro	Ile	Cys	Thr	Glu	40	Gly	Val	Val	Ser	Val	45
Ser	Trp	Gly	Glu	50	Asn	Thr	Val	Met	Ser	55	Cys	Asn	Ile	Ser	Asn	60
Phe	Ser	His	Val	65	Asn	Ile	Lys	Leu	Arg	70	Ala	His	Gly	Gln	Glu	75
Ala	Ile	Phe	Asn	80	Val	Ala	Pro	Gly	Tyr	85	Phe	Ser	Arg	Asp	Gly	90
Trp	Gln	Leu	Gln	95	Val	Gln	Gly	Gly	Val	100	Ala	Gln	Leu	Val	Ile	Lys
Gly	Ala	Arg	Asp	110	Ser	His	Ala	Gly	Leu	115	Tyr	Met	Trp	His	Leu	120
Gly	His	Gln	Arg	125	Asn	Asn	Arg	Gln	Val	130	Thr	Leu	Glu	Val	Ser	135
Ala	Glu	Pro	Gln	140	Ser	Ala	Pro	Asp	Thr	145	Gly	Phe	Trp	Pro	Val	150
Ala	Val	Val	Thr	155	Ala	Val	Phe	Ile	Leu	160	Leu	Val	Ala	Leu	Val	165
Phe	Ala	Trp	Tyr	170	Arg	Cys	Arg	Cys	Ser	175	Gln	Arg	Arg	Glu	Lys	180
Lys	Phe	Phe	Leu	185	Leu	Glu	Pro	Gln	Met	190	Lys	Val	Ala	Ala	Leu	195
Ala	Gly	Ala	Gln	200	Gln	Gly	Leu	Ser	Arg	205	Ala	Ser	Ala	Glu	Leu	210
Thr	Pro	Asp	Ser	215	Glu	Pro	Thr	Pro	Arg	220	Pro	Leu	Ala	Leu	Val	225
Lys	Pro	Ser	Pro	230	Leu	Gly	Ala	Leu	Glu	235	Leu	Leu	Ser	Pro	Gln	240
Leu	Phe	Pro	Tyr	245	Ala	Ala	Asp	Pro								

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: STOMTUT02

(B) CLONE: 1750632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33 :

Met	Leu	Glu	Glu	Gly	Ser	Phe	Arg	Gly	Arg	Thr	Ala	Asp	Phe	Val	5	10	15
Phe	Met	Phe	Leu	Phe	Gly	Gly	Val	Leu	Met	Thr	Val	Ser	Phe	Pro	20	25	30
Gln	Ala	Leu	Glu	Pro	Arg	Ala	Arg	Ala	Pro	Arg	Arg	Pro	Ala	Cys	35	40	45
Val	Gly	Pro	Gly	Ala	Asn	Thr	Ala	Met	Pro	Glu	Arg	Asp	Thr	Val	50	55	60
Ala	Val	Ser	Ser	Leu	Ala	Pro	Phe	Leu	Pro	Trp	Ala	Leu	Met	Gly	65	70	75
Phe	Ser	Leu	Leu	Leu	Gly	Asn	Ser	Ile	Leu	Val	Asp	Leu	Leu	Gly	80	85	90
Ile	Ala	Val	Gly	His	Ile	Tyr	Tyr	Phe	Leu	Glu	Asp	Val	Phe	Pro	95	100	105
Asn	Gln	Pro	Gly	Gly	Lys	Arg	Leu	Leu	Gln	Thr	Pro	Gly	Phe	Leu	110	115	120
Lys	Leu	Leu	Leu	Asp	Ala	Pro	Ala	Glu	Asp	Pro	Asn	Tyr	Leu	Pro	125	130	135
Leu	Pro	Glu	Glu	Gln	Pro	Gly	Pro	His	Leu	Pro	Pro	Pro	Gln	Gln	140	145	150

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34 :

Met	Trp	Ala	Leu	Gly	Gln	Ala	Gly	Phe	Ala	Asn	Leu	Thr	Glu	Gly	5	10	15
Leu	Lys	Val	Trp	Leu	Gly	Ile	Met	Leu	Pro	Val	Leu	Gly	Ile	Lys	20	25	30
Ser	Leu	Ser	Pro	Phe	Ala	Ile	Thr	Tyr	Leu	Asp	Arg	Leu	Leu	Leu	35	40	45
Met	His	Pro	Asn	Leu	Thr	Lys	Gly	Phe	Gly	Met	Ile	Gly	Pro	Lys	50	55	60
Asp	Phe	Phe	Pro	Leu	Leu	Asp	Phe	Ala	Tyr	Met	Pro	Asn	Asn	Ser	65	70	75
Leu	Thr	Pro	Ser	Leu	Gln	Glu	Gln	Leu	Cys	Gln	Leu	Tyr	Pro	Arg	80	85	90
Leu	Lys	Met	Leu	Ala	Phe	Gly	Ala	Lys	Pro	Asp	Ser	Thr	Leu	His	95	100	105
Thr	Tyr	Phe	Pro	Ser	Phe	Leu	Ser	Arg	Ala	Thr	Pro	Ser	Cys	Pro	110	115	120

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Pro	Glu	Met	Lys	Lys	Glu	Leu	Leu	Ser	Ser	Leu	Thr	Glu	Cys	Leu	
				125					130					135	
Thr	Val	Asp	Pro	Leu	Ser	Ala	Ser	Val	Trp	Arg	Gln	Leu	Tyr	Pro	
				140					145					150	
Lys	His	Leu	Ser	Gln	Ser	Ser	Leu	Leu	Leu	Glu	His	Leu	Leu	Ser	
				155					160					165	
Ser	Trp	Glu	Gln	Ile	Pro	Lys	Lys	Val	Gln	Lys	Ser	Leu	Gln	Glu	
				170					175					180	
Thr	Ile	Gln	Ser	Leu	Lys	Leu	Thr	Asn	Gln	Glu	Leu	Leu	Arg	Lys	
				185					190					195	
Gly	Ser	Ser	Asn	Asn	Gln	Asp	Val	Val	Thr	Cys	Asp	Met	Ala	Cys	
				200					205					210	
Lys	Gly	Leu	Leu	Gln	Gln	Val	Gln	Gly	Pro	Arg	Leu	Pro	Trp	Thr	
				215					220					225	
Arg	Leu	Leu	Leu	Leu	Leu	Leu	Val	Phe	Ala	Val	Gly	Phe	Leu	Cys	
				230					235					240	
His	Asp	Leu	Arg	Ser	His	Ser	Ser	Phe	Gln	Ala	Ser	Leu	Thr	Gly	
				245					250					255	
Arg	Leu	Leu	Arg	Ser	Ser	Gly	Phe	Leu	Pro	Ala	Ser	Gln	Gln	Ala	
				260					265					270	
Cys	Ala	Lys	Leu	Tyr	Ser	Tyr	Ser	Leu	Gln	Gly	Tyr	Ser	Trp	Leu	
				275					280					285	
Gly	Glu	Thr	Leu	Pro	Leu	Trp	Gly	Ser	His	Leu	Leu	Thr	Val	Val	
				290					295					300	
Arg	Pro	Ser	Leu	Gln	Leu	Ala	Trp	Ala	His	Thr	Asn	Ala	Thr	Val	
				305					310					315	
Ser	Phe	Leu	Ser	Ala	His	Cys	Ala	Ser	His	Leu	Ala	Trp	Phe	Gly	
				320					325					330	
Asp	Ser	Leu	Thr	Ser	Leu	Ser	Gln	Arg	Leu	Gln	Ile	Gln	Leu	Pro	
				335					340					345	
Asp	Ser	Val	Asn	Gln	Leu	Leu	Arg	Tyr	Leu	Arg	Glu	Leu	Pro	Leu	
				350					355					360	
Leu	Phe	His	Gln	Asn	Val	Leu	Leu	Pro	Leu	Trp	His	Leu	Leu	Leu	
				365					370					375	
Glu	Ala	Leu	Ala	Trp	Ala	Gln	Glu	His	Cys	His	Glu	Ala	Cys	Arg	
				380					385					390	
Gly	Glu	Val	Thr	Trp	Asp	Cys	Met	Lys	Thr	Gln	Leu	Ser	Glu	Ala	
				395					400					405	
Val	His	Trp	Thr	Trp	Leu	Cys	Leu	Gln	Asp	Ile	Thr	Val	Ala	Phe	
				410					415					420	
Leu	Asp	Trp	Ala	Leu	Ala	Leu	Ile	Ser	Gln	Gln					
				425					430						

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT20
- (B) CLONE: 1818761



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35 :

Met	Gln	Trp	Leu	Arg	Val	Arg	Glu	Ser	Pro	Gly	Glu	Ala	Thr	Gly	5	10	15
His	Arg	Val	Thr	Met	Gly	Thr	Ala	Ala	Leu	Gly	Pro	Val	Trp	Ala	20	25	30
Ala	Leu	Leu	Leu	Phe	Leu	Leu	Met	Cys	Glu	Ile	Pro	Met	Val	Glu	35	40	45
Leu	Thr	Phe	Asp	Arg	Ala	Val	Ala	Ser	Gly	Cys	Gln	Arg	Cys	Cys	50	55	60
Asp	Ser	Glu	Asp	Pro	Leu	Asp	Pro	Ala	His	Val	Ser	Ser	Ala	Ser	65	70	75
Ser	Ser	Gly	Arg	Pro	His	Ala	Leu	Pro	Glu	Ile	Arg	Pro	Tyr	Ile	80	85	90
Asn	Ile	Thr	Ile	Leu	Lys	Gly	Asp	Lys	Gly	Asp	Pro	Gly	Pro	Met	95	100	105
Gly	Leu	Pro	Gly	Tyr	Met	Gly	Arg	Glu	Gly	Pro	Gln	Gly	Glu	Pro	110	115	120
Gly	Pro	Gln	Gly	Ser	Lys	Gly	Asp	Lys	Gly	Glu	Met	Gly	Ser	Pro	125	130	135
Gly	Ala	Pro	Cys	Gln	Lys	Arg	Phe	Phe	Ala	Phe	Ser	Val	Gly	Arg	140	145	150
Lys	Thr	Ala	Leu	His	Ser	Gly	Glu	Asp	Phe	Gln	Thr	Leu	Leu	Phe	155	160	165
Glu	Arg	Val	Phe	Val	Asn	Leu	Asp	Gly	Cys	Phe	Asp	Met	Ala	Thr	170	175	180
Gly	Gln	Phe	Ala	Ala	Pro	Leu	Arg	Gly	Ile	Tyr	Phe	Phe	Ser	Leu	185	190	195
Asn	Val	His	Ser	Trp	Asn	Tyr	Lys	Glu	Thr	Tyr	Val	His	Ile	Met	200	205	210
His	Asn	Gln	Lys	Glu	Ala	Val	Ile	Leu	Tyr	Ala	Gln	Pro	Ser	Glu	215	220	225
Arg	Ser	Ile	Met	Gln	Ser	Gln	Ser	Val	Met	Leu	Asp	Leu	Ala	Tyr	230	235	240
Gly	Asp	Arg	Val	Trp	Val	Arg	Leu	Phe	Lys	Arg	Gln	Arg	Glu	Asn	245	250	255
Ala	Ile	Tyr	Ser	Asn	Asp	Phe	Asp	Thr	Tyr	Ile	Thr	Phe	Ser	Gly	260	265	270
His	Leu	Ile	Lys	Ala	Glu	Asp	Asp								275		

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GBLATUT01
- (B) CLONE: 1824469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36 :

Met	Glu	Glu	Lys	Arg	Arg	Arg	Ala	Arg	Val	Gln	Gly	Ala	Trp	Ala	5	10	15
Ala	Pro	Val	Lys	Ser	Gln	Ala	Ile	Ala	Gln	Pro	Ala	Thr	Thr	Ala			

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				20					25					30
Lys	Ser	His	Leu	His	Gln	Lys	Pro	Gly	Gln	Thr	Trp	Lys	Asn	Lys
				35					40					45
Glu	His	His	Leu	Ser	Asp	Arg	Glu	Phe	Val	Phe	Lys	Glu	Pro	Gln
				50					55					60
Gln	Val	Val	Arg	Arg	Ala	Pro	Glu	Pro	Arg	Val	Ile	Asp	Arg	Glu
				65					70					75
Gly	Val	Tyr	Glu	Ile	Ser	Leu	Ser	Pro	Thr	Gly	Val	Ser	Arg	Val
				80					85					90
Cys	Leu	Tyr	Pro	Gly	Phe	Val	Asp	Val	Lys	Glu	Ala	Asp	Trp	Ile
				95					100					105
Leu	Glu	Gln	Leu	Cys	Gln	Asp	Val	Pro	Trp	Lys	Gln	Arg	Thr	Gly
				110					115					120
Ile	Arg	Glu	Asp	Ile	Thr	Tyr	Gln	Gln	Pro	Arg	Leu	Thr	Ala	Trp
				125					130					135
Tyr	Gly	Glu	Leu	Pro	Tyr	Thr	Tyr	Ser	Arg	Ile	Thr	Met	Glu	Pro
				140					145					150
Asn	Pro	His	Trp	His	Pro	Val	Leu	Arg	Thr	Leu	Lys	Asn	Arg	Ile
				155					160					165
Glu	Glu	Asn	Thr	Gly	His	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Asn	Leu
				170					175					180
Tyr	Arg	Asn	Glu	Lys	Asp	Ser	Val	Asp	Trp	His	Ser	Asp	Asp	Glu
				185					190					195
Pro	Ser	Leu	Gly	Arg	Cys	Pro	Ile	Ile	Ala	Ser	Leu	Ser	Phe	Gly
				200					205					210
Ala	Thr	Arg	Thr	Phe	Glu	Met	Arg	Lys	Lys	Pro	Pro	Pro	Glu	Glu
				215					220					225
Asn	Gly	Asp	Tyr	Thr	Tyr	Val	Glu	Arg	Val	Lys	Ile	Pro	Leu	Asp
				230					235					240
His	Gly	Thr	Leu	Leu	Ile	Met	Glu	Gly	Ala	Thr	Gln	Ala	Asp	Trp
				245					250					255
Gln	His	Arg	Val	Pro	Lys	Glu	Tyr	His	Ser	Arg	Glu	Pro	Arg	Val
				260					265					270
Asn	Leu	Thr	Phe	Arg	Thr	Val	Tyr	Pro	Asp	Pro	Arg	Gly	Ala	Pro
				275					280					285
Trp														

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT19
- (B) CLONE: 1864292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37 :

Met	Lys	Met	Glu	Glu	Ala	Val	Gly	Lys	Val	Glu	Glu	Leu	Ile	Glu
				5					10					15
Ser	Glu	Ala	Pro	Pro	Lys	Ala	Ser	Glu	Gln	Glu	Thr	Ala	Lys	Glu
				20					25					30
Glu	Asp	Gly	Ser	Val	Glu	Leu	Glu	Ser	Gln	Val	Gln	Lys	Asp	Gly
				35					40					45

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Val	Ala	Asp	Ser	Thr	Val	Ile	Ser	Ser	Met	Pro	Cys	Leu	Leu	Met
				50					55					60
Glu	Leu	Arg	Arg	Asp	Ser	Ser	Glu	Ser	Gln	Leu	Ala	Ser	Thr	Glu
				65					70					75
Ser	Asp	Lys	Pro	Thr	Thr	Gly	Arg	Val	Tyr	Glu	Ser	Asp	Pro	Ser
				80					85					90
Asn	His	Cys	Met	Leu	Ser	Pro	Ser	Ser	Ser	Gly	His	Leu	Ala	Asp
				95					100					105
Ser	Asp	Thr	Leu	Ser	Ser	Ala	Glu	Glu	Asn	Glu	Pro	Ser	Gln	Ala
				110					115					120
Glu	Thr	Ala	Val	Glu	Gly	Asp	Pro	Ser	Gly	Val	Ser	Gly	Ala	Thr
				125					130					135
Val	Gly	Arg	Lys	Ser	Arg	Arg	Ser	Arg	Ser	Glu	Ser	Glu	Thr	Ser
				140					145					150
Thr	Met	Ala	Ala	Lys	Lys	Asn	Arg	Gln	Ser	Ser	Asp	Lys	Gln	Asn
				155					160					165
Gly	Arg	Val	Ala	Lys	Val	Lys	Gly	His	Arg	Ser	Gln	Lys	His	Lys
				170					175					180
Glu	Arg	Ile	Arg	Leu	Leu	Arg	Gln	Lys	Arg	Glu	Ala	Ala	Ala	Arg
				185					190					195
Lys	Lys	Tyr	Asn	Leu	Leu	Gln	Asp	Ser	Ser	Thr	Ser	Asp	Ser	Asp
				200					205					210
Leu	Thr	Cys	Asp	Ser	Ser	Thr	Ser	Ser	Ser	Asp	Asp	Asp	Glu	Glu
				215					220					225
Val	Ser	Gly	Ser	Ser	Lys	Thr	Ile	Thr	Ala	Glu	Ile	Pro	Asp	Gly
				230					235					240
Pro	Pro	Val	Val	Ala	His	Tyr	Asp	Met	Ser	Asp	Thr	Asn	Ser	Asp
				245					250					255
Pro	Glu	Val	Val	Asn	Val	Asp	Asn	Leu	Leu	Ala	Ala	Ala	Val	Val
				260					265					270
Gln	Glu	His	Ser	Asn	Ser	Val	Gly	Gly	Gln	Asp	Thr	Gly	Ala	Thr
				275					280					285
Trp	Arg	Thr	Ser	Gly	Leu	Leu	Glu	Glu	Leu	Asn	Ala	Glu	Ala	Gly
				290					295					300
His	Leu	Asp	Pro	Gly	Phe	Leu	Ala	Ser	Asp	Lys	Thr	Ser	Ala	Gly
				305					310					315
Asn	Ala	Pro	Leu	Asn	Glu	Glu	Ile	Asn	Ile	Ala	Ser	Ser	Asp	Ser
				320					325					330
Glu	Val	Glu	Ile	Val	Gly	Val	Gln	Glu	His	Ala	Arg	Cys	Val	His
				335					340					345
Pro	Arg	Gly	Gly	Val	Ile	Gln	Ser	Val	Ser	Ser	Trp	Lys	His	Gly
				350					355					360
Ser	Gly	Thr	Gln	Tyr	Val	Ser	Thr	Arg	Gln	Thr	Gln	Ser	Trp	Thr
				365					370					375
Ala	Val	Thr	Pro	Gln	Gln	Thr	Trp	Ala	Ser	Pro	Ala	Glu	Val	Val
				380					385					390
Asp	Leu	Thr	Leu	Asp	Glu	Asp	Ser	Arg	Arg	Lys	Tyr	Leu	Leu	
				395					400					

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

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(A) LIBRARY: THP1NOT01

(B) CLONE: 1866437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38 :

Met	Phe	Val	Gln	Glu	Glu	Lys	Ile	Phe	Ala	Gly	Lys	Val	Leu	Arg	5	10	15
Leu	His	Ile	Cys	Ala	Ser	Asp	Gly	Ala	Glu	Trp	Leu	Glu	Glu	Ala	20	25	30
Thr	Glu	Asp	Thr	Ser	Val	Glu	Lys	Leu	Lys	Glu	Arg	Cys	Leu	Lys	35	40	45
His	Cys	Ala	His	Gly	Ser	Leu	Glu	Asp	Pro	Lys	Ser	Ile	Thr	His	50	55	60
His	Lys	Leu	Ile	His	Ala	Ala	Ser	Glu	Arg	Val	Leu	Ser	Asp	Ala	65	70	75
Arg	Thr	Ile	Leu	Glu	Glu	Asn	Ile	Gln	Asp	Gln	Asp	Val	Leu	Leu	80	85	90
Leu	Lys	Lys	Lys	Arg	Ala	Pro	Ser	Pro	Leu	Pro	Lys	Met	Ala	Asp	95	100	105
Val	Ser	Ala	Glu	Glu	Lys	Lys	Lys	Gln	Asp	Gln	Lys	Ala	Pro	Asp	110	115	120
Lys	Glu	Ala	Ile	Leu	Arg	Ala	Thr	Ala	Asn	Leu	Pro	Ser	Tyr	Asn	125	130	135
Met	Asp	Arg	Ala	Ala	Val	Gln	Thr	Asn	Met	Arg	Asp	Phe	Gln	Thr	140	145	150
Glu	Leu	Arg	Lys	Ile	Leu	Val	Ser	Leu	Ile	Glu	Val	Ala	Gln	Lys	155	160	165
Leu	Leu	Ala	Leu	Asn	Pro	Asp	Ala	Val	Glu	Leu	Phe	Lys	Lys	Ala	170	175	180
Asn	Ala	Met	Leu	Asp	Glu	Asp	Glu	Asp	Glu	Arg	Val	Asp	Glu	Ala	185	190	195
Ala	Leu	Arg	Gln	Leu	Thr	Glu	Met	Gly	Phe	Pro	Glu	Asn	Arg	Ala	200	205	210
Thr	Lys	Ala	Leu	Gln	Leu	Asn	His	Met	Ser	Val	Pro	Gln	Ala	Met	215	220	225
Glu	Trp	Leu	Ile	Glu	His	Ala	Glu	Asp	Pro	Thr	Ile	Asp	Thr	Pro	230	235	240
Leu	Pro	Gly	Gln	Ala	Pro	Pro	Glu	Ala	Glu	Gly	Ala	Thr	Ala	Ala	245	250	255
Ala	Ser	Glu	Ala	Ala	Ala	Gly	Ala	Ser	Ala	Thr	Asp	Glu	Glu	Ala	260	265	270
Arg	Asp	Glu	Leu	Thr	Glu	Ile	Phe	Lys	Lys	Ile	Arg	Arg	Lys	Arg	275	280	285
Glu	Phe	Arg	Ala	Asp	Ala	Arg	Ala	Val	Ile	Ser	Leu	Met	Glu	Met	290	295	300
Gly	Phe	Asp	Glu	Lys	Glu	Val	Ile	Asp	Ala	Leu	Arg	Val	Asn	Asn	305	310	315
Asn	Gln	Gln	Asn	Ala	Ala	Cys	Glu	Trp	Leu	Leu	Gly	Asp	Arg	Lys	320	325	330
Pro	Ser	Pro	Glu	Glu	Leu	Asp	Lys	Gly	Ile	Asp	Pro	Asp	Ser	Pro	335	340	345
Leu	Phe	Gln	Ala	Ile	Leu	Asp	Asn	Pro	Val	Val	Gln	Leu	Gly	Leu	350	355	360
Thr	Asn	Pro	Lys	Thr	Leu	Leu	Ala	Phe	Glu	Asp	Met	Leu	Glu	Asn	365	370	375
Pro	Leu	Asn	Ser	Thr	Gln	Trp	Met	Asn	Asp	Pro	Glu	Thr	Gly	Pro	380	385	390
Val	Met	Leu	Gln	Ile	Ser	Arg	Ile	Phe	Gln	Thr	Leu	Asn	Arg	Thr	395	400	405

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SKINBIT01
- (B) CLONE: 1871375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39 :

Met	Val	Met	His	Asn	Ser	Asp	Pro	Asn	Leu	His	Leu	Leu	Ala	Glu	5	10	15
Gly	Ala	Pro	Ile	Asp	Trp	Gly	Glu	Glu	Tyr	Ser	Asn	Ser	Gly	Gly	20	25	30
Gly	Gly	Ser	Pro	Ala	Pro	Ala	Pro	Arg	Ser	Gln	Pro	Pro	Ser	Arg	35	40	45
Lys	Ser	Asp	Gly	Ala	Pro	Ser	Arg	Trp	Ser	Leu	Trp	Ser	Arg	Met	50	55	60
Arg	Arg	Trp	Gly	Cys	Pro	Leu	Arg	Leu	Ala	Leu	Ser	His	His	His	65	70	75
Leu	Arg	Pro	Arg	Thr	Val	Ser	Leu	Arg	Ser	Glu	Ala	Cys	Trp	Pro	80	85	90
Lys	Val	Cys	Gly	Leu	Arg	Ala	Pro	His	Gln	Pro	Ala	Pro	Cys	Ser	95	100	105
Thr	Gly	Pro	Pro	Leu	Gly	Arg	Val	Pro	Ser	Leu	Arg	Pro	Pro	Pro	110	115	120
Arg	Pro	Pro	Arg	Arg	Leu	Pro	His	Pro	Ser	Ser	Ile	Ser	Cys	Leu	125	130	135
Glu	Arg	Leu	Trp	Thr	Leu	Gly	Pro	Pro	Ser	Pro	Ala	Thr	Arg	Arg	140	145	150
Leu	Glu	Ser	Arg	Cys	Pro	Ala	Pro	Ala	Ala	Thr	Pro	Pro	Ser	Thr	155	160	165
Pro	Pro	Pro	Arg	Xaa	Xaa	Phe	Lys	Gly	Cys	Lys	Asn				170	175	

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LEUKNOT03
- (B) CLONE: 1880830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40 :

Met	Ile	Thr	Cys	Arg	Val	Cys	Gln	Ser	Leu	Ile	Asn	Val	Glu	Gly	5	10	15
Lys	Met	His	Gln	His	Val	Val	Lys	Cys	Gly	Val	Cys	Asn	Glu	Ala	20	25	30

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Thr	Pro	Ile	Lys	Asn	Ala	Pro	Pro	Gly	Lys	Lys	Tyr	Val	Arg	Cys	
				35					40					45	
Pro	Cys	Asn	Cys	Leu	Leu	Ile	Cys	Lys	Val	Thr	Ser	Gln	Arg	Ile	
				50					55					60	
Ala	Cys	Pro	Arg	Pro	Tyr	Cys	Lys	Arg	Ile	Ile	Asn	Leu	Gly	Pro	
				65					70					75	
Val	His	Pro	Gly	Pro	Leu	Ser	Pro	Glu	Pro	Gln	Pro	Met	Gly	Val	
				80					85					90	
Arg	Val	Ile	Cys	Gly	His	Cys	Lys	Asn	Thr	Phe	Leu	Trp	Thr	Glu	
				95					100					105	
Phe	Thr	Asp	Arg	Thr	Leu	Ala	Arg	Cys	Pro	His	Cys	Arg	Lys	Val	
				110					115					120	
Ser	Ser	Ile	Gly	Arg	Arg	Tyr	Pro	Arg	Lys	Arg	Cys	Ile	Cys	Cys	
				125					130					135	
Phe	Leu	Leu	Gly	Leu	Leu	Leu	Ala	Val	Thr	Ala	Thr	Gly	Leu	Ala	
				140					145					150	
Phe	Gly	Thr	Trp	Lys	His	Ala	Arg	Arg	Tyr	Gly	Gly	Ile	Tyr	Ala	
				155					160					165	
Ala	Trp	Ala	Phe	Val	Ile	Leu	Leu	Ala	Val	Leu	Cys	Leu	Gly	Arg	
				170					175					180	
Ala	Leu	Tyr	Trp	Ala	Cys	Met	Lys	Val	Ser	His	Pro	Val	Gln	Asn	
				185					190					195	
Phe	Ser														

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARNOT07
- (B) CLONE: 1905325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41 :

Met	Leu	Lys	Asp	Ile	Ile	Lys	Glu	Tyr	Thr	Asp	Val	Tyr	Pro	Glu	
				5					10					15	
Ile	Ile	Glu	Arg	Ala	Gly	Tyr	Ser	Leu	Glu	Lys	Val	Phe	Gly	Ile	
				20					25					30	
Gln	Leu	Lys	Glu	Ile	Asp	Lys	Asn	Asp	His	Leu	Tyr	Ile	Leu	Leu	
				35					40					45	
Ser	Thr	Leu	Glu	Pro	Thr	Asp	Ala	Gly	Ile	Leu	Gly	Thr	Thr	Lys	
				50					55					60	
Asp	Ser	Pro	Lys	Leu	Gly	Leu	Leu	Met	Val	Leu	Leu	Ser	Ile	Ile	
				65					70					75	
Phe	Met	Asn	Gly	Asn	Arg	Ser	Ser	Glu	Ala	Val	Ile	Trp	Glu	Val	
				80					85					90	
Leu	Arg	Lys	Leu	Gly	Leu	Arg	Pro	Gly	Ile	His	His	Ser	Leu	Phe	
				95					100					105	
Gly	Asp	Val	Lys	Lys	Leu	Ile	Thr	Asp	Glu	Phe	Val	Lys	Gln	Lys	
				110					115					120	
Tyr	Leu	Asp	Tyr	Ala	Arg	Val	Pro	Asn	Ser	Asn	Pro	Pro	Glu	Tyr	
				125					130					135	
Glu	Phe	Phe	Trp	Gly	Leu	Arg	Ser	Tyr	Tyr	Glu	Thr	Ser	Lys	Met	
				140					145					150	
Lys	Val	Leu	Lys	Phe	Ala	Cys	Lys	Val	Gln	Lys	Lys	Asp	Pro	Lys	

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Glu	Trp	Ala	Ala	Gln	Tyr	Arg	Glu	Ala	Met	Glu	Ala	Asp	Leu	Lys
155									160					165
Ala	Ala	Ala	Glu	Ala	Ala	Ala	Glu	Ala	Lys	Ala	Arg	Ala	Glu	Ile
170									175					180
Arg	Ala	Arg	Met	Gly	Ile	Gly	Leu	Gly	Ser	Glu	Asn	Ala	Ala	Gly
185									190					195
Pro	Cys	Asn	Trp	Asp	Glu	Ala	Asp	Ile	Gly	Pro	Trp	Ala	Lys	Ala
200									205					210
Arg	Ile	Gln	Ala	Gly	Ala	Glu	Ala	Lys	Ala	Lys	Ala	Gln	Glu	Ser
215									220					225
Gly	Ser	Ala	Ser	Thr	Gly	Ala	Ser	Thr	Ser	Thr	Asn	Asn	Ser	Ala
230									235					240
Ser	Ala	Ser	Ala	Ser	Thr	Ser	Gly	Gly	Phe	Ser	Ala	Gly	Ala	Ser
245									250					255
Leu	Thr	Ala	Thr	Leu	Thr	Phe	Gly	Leu	Phe	Ala	Gly	Leu	Gly	Gly
260									265					270
Ala	Gly	Ala	Ser	Thr	Ser	Gly	Ser	Ser	Gly	Ala	Cys	Gly	Phe	Ser
275									280					285
Tyr	Lys								295					300

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT01
- (B) CLONE: 1919931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42 :

Met	Arg	Thr	Leu	Glu	Asn	Gln	Gly	Phe	Lys	Ile	Leu	Pro	Phe	Leu
5									10					15
Gly	Val	Lys	Glu	Val	Trp	Gln	Lys	Gln	Asn	Lys	Leu	Ile	Ser	Arg
20									25					30
Phe	Ile	Thr	Cys	Gln	Phe	Phe	Leu	Tyr	Asn	Phe	Leu	Asp	Ser	Gly
35									40					45
Ser	Ile	Trp	Val	Gln	Ala	Asp	Phe	Pro	Pro	Ile	Leu	Gln	Cys	Gly
50									55					60
Cys	Phe	Leu	Phe	His	Pro	Trp	Thr	Leu	Gln	Glu	Ile	Ala	Pro	Cys
65									70					75
Phe	Cys	Leu	Cys	Ile	Thr	Glu	Lys	Gly	Ser	Met	Lys	Val	Ala	Gln
80									85					90
Val	Arg	Pro	Phe	His	Cys	Pro	Pro	Gly	Ala	Gly	Phe	Ala	Leu	Pro
95									100					105
Ile	Leu	Gly	Leu	Leu	Gln	Gly	Leu	Val	Ile	Leu	His	Ser	Pro	Leu
110									115					120
His	Ile	Ser	Gln	Val	Ser	Ala	Gln	Lys	Ser	Pro	Phe	Gly	Gly	Val
125									130					135
Ser	Thr	Cys	His	Cys	Val	Cys	Lys	Ser	Ser	Phe	Ser	Phe	Phe	Leu
140									145					150
Ala	His	Leu	Thr	Leu	Val	Met	Ser	Leu	Ile	Thr	Thr	Thr	Ile	
155									160					

## (2) INFORMATION FOR SEQ ID NO: 43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT04
- (B) CLONE: 1969426

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43 :

Met	Ser	Pro	Thr	Leu	Ser	Ser	Ile	Thr	Gln	Gly	Val	Pro	Leu	Asp	5	10	15
Thr	Ser	Lys	Leu	Ser	Thr	Asp	Gln	Arg	Leu	Pro	Pro	Tyr	Pro	Tyr	20	25	30
Ser	Ser	Pro	Ser	Leu	Val	Leu	Pro	Thr	Gln	Pro	His	Thr	Pro	Lys	35	40	45
Ser	Leu	Gln	Gln	Pro	Gly	Leu	Pro	Ser	Gln	Ser	Cys	Ser	Val	Gln	50	55	60
Ser	Ser	Gly	Gly	Gln	Pro	Pro	Gly	Arg	Gln	Ser	His	Tyr	Gly	Thr	65	70	75
Pro	Tyr	Pro	Pro	Gly	Pro	Ser	Gly	His	Gly	Gln	Gln	Ser	Tyr	His	80	85	90
Arg	Pro	Met	Ser	Asp	Phe	Asn	Leu	Gly	Asn	Leu	Glu	Gln	Phe	Ser	95	100	105
Met	Glu	Ser	Pro	Ser	Ala	Ser	Leu	Val	Leu	Asp	Pro	Pro	Gly	Phe	110	115	120
Ser	Glu	Gly	Pro	Gly	Phe	Leu	Gly	Gly	Glu	Gly	Pro	Met	Gly	Gly	125	130	135
Pro	Gln	Asp	Pro	His	Thr	Phe	Asn	His	Gln	Asn	Leu	Thr	His	Cys	140	145	150
Ser	Arg	His	Gly	Ser	Gly	Pro	Asn	Ile	Ile	Leu	Thr	Gly	Asp	Ser	155	160	165
Ser	Pro	Gly	Phe	Ser	Lys	Glu	Ile	Ala	Ala	Ala	Leu	Ala	Gly	Val	170	175	180
Pro	Gly	Phe	Glu	Val	Ser	Ala	Ala	Gly	Leu	Glu	Leu	Gly	Leu	Gly	185	190	195
Leu	Glu	Asp	Glu	Leu	Arg	Met	Glu	Pro	Leu	Gly	Leu	Glu	Gly	Leu	200	205	210
Asn	Met	Leu	Ser	Asp	Pro	Cys	Ala	Leu	Leu	Pro	Asp	Pro	Ala	Val	215	220	225
Glu	Glu	Ser	Phe	Arg	Ser	Asp	Arg	Leu	Gln						230	235	

## (2) INFORMATION FOR SEQ ID NO: 44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UCMCL5T01



(B) CLONE: 1969948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44 :

Met	Asn	Tyr	Phe	Pro	Leu	Ala	Pro	Phe	Asn	Gln	Leu	Leu	Gln	Lys	5	10	15
Asp	Ile	Ile	Ser	Glu	Leu	Leu	Thr	Ser	Asp	Asp	Met	Lys	Asn	Ala	20	25	30
Tyr	Lys	Leu	His	Thr	Leu	Asp	Thr	Cys	Leu	Lys	Leu	Asp	Asp	Thr	35	40	45
Val	Tyr	Leu	Arg	Asp	Ile	Ala	Leu	Ser	Leu	Pro	Gln	Leu	Pro	Arg	50	55	60
Glu	Leu	Pro	Ser	Ser	His	Thr	Asn	Ala	Lys	Val	Ala	Glu	Val	Leu	65	70	75
Ser	Ser	Leu	Leu	Gly	Gly	Glu	Gly	His	Phe	Ser	Lys	Asp	Val	His	80	85	90
Leu	Pro	His	Asn	Tyr	His	Ile	Asp	Phe	Glu	Ile	Arg	Met	Asp	Thr	95	100	105
Asn	Arg	Asn	Gln	Val	Leu	Pro	Leu	Ser	Asp	Val	Asp	Thr	Thr	Ser	110	115	120
Ala	Thr	Asp	Ile	Gln	Arg	Val	Ala	Val	Leu	Cys	Val	Ser	Arg	Ser	125	130	135
Ala	Tyr	Cys	Leu	Gly	Ser	Ser	His	Pro	Arg	Gly	Phe	Leu	Ala	Met	140	145	150
Lys	Met	Arg	His	Leu	Asn	Ala	Met	Gly	Phe	His	Val	Ile	Leu	Val	155	160	165
Asn	Asn	Trp	Glu	Met	Asp	Lys	Leu	Glu	Met	Glu	Asp	Ala	Val	Thr	170	175	180
Phe	Leu	Lys	Thr	Lys	Ile	Tyr	Ser	Val	Glu	Ala	Leu	Pro	Val	Ala	185	190	195
Ala	Val	Asn	Val	Gln	Ser	Thr	Gln								200		

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGAST01
- (B) CLONE: 1988911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45 :

Met	Glu	Arg	Gly	Asn	Val	Leu	Ser	Arg	Ala	Pro	Ser	Arg	Ala	His	5	10	15
Gly	Thr	His	Phe	Gly	Asp	Asp	Arg	Phe	Glu	Asp	Leu	Glu	Glu	Ala	20	25	30
Asn	Pro	Phe	Ser	Phe	Arg	Glu	Phe	Leu	Lys	Thr	Lys	Asn	Leu	Gly	35	40	45
Leu	Ser	Lys	Glu	Asp	Pro	Ala	Ser	Arg	Ile	Tyr	Ala	Lys	Glu	Ala	50	55	60
Ser	Arg	His	Ser	Leu	Gly	Leu	Asp	His	Asn	Ser	Pro	Pro	Ser	Gln	65	70	75
Thr	Gly	Gly	Tyr	Gly	Leu	Glu	Tyr	Gln	Gln	Pro	Phe	Phe	Glu	Asp			

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Pro	Thr	Gly	Ala	Gly	Asp	Leu	Leu	Asp	Glu	Glu	Glu	Asp	Glu	Asp	80	85	90
Thr	Gly	Trp	Ser	Gly	Ala	Tyr	Leu	Pro	Ser	Ala	Ile	Glu	Gln	Thr	95	100	105
His	Pro	Glu	Arg	Val	Pro	Ala	Gly	Thr	Ser	Pro	Cys	Ser	Thr	Tyr	110	115	120
Leu	Ser	Phe	Phe	Ser	Thr	Pro	Ser	Glu	Leu	Ala	Gly	Pro	Glu	Ser	125	130	135
Leu	Pro	Ser	Trp	Ala	Leu	Ser	Asp	Thr	Asp	Ser	Arg	Val	Ser	Pro	140	145	150
Ala	Ser	Pro	Ala	Gly	Ser	Pro	Ser	Ala	Asp	Phe	Ala	Val	His	Gly	155	160	165
Glu	Ser	Leu	Gly	Asp	Arg	His	Leu	Arg	Thr	Leu	Gln	Ile	Ser	Tyr	170	175	180
Asp	Ala	Leu	Lys	Asp	Glu	Asn	Ser	Lys	Leu	Arg	Arg	Lys	Leu	Asn	185	190	195
Glu	Val	Gln	Ser	Phe	Ser	Glu	Ala	Gln	Thr	Glu	Met	Val	Arg	Thr	200	205	210
Leu	Glu	Arg	Lys	Leu	Glu	Ala	Lys	Met	Ile	Lys	Glu	Glu	Ser	Asp	215	220	225
Tyr	His	Asp	Leu	Glu	Ser	Val	Val	Gln	Gln	Val	Glu	Gln	Asn	Leu	230	235	240
Glu	Leu	Met	Thr	Lys	Arg	Ala	Val	Lys	Ala	Glu	Asn	His	Val	Val	245	250	255
Lys	Leu	Lys	Gln	Glu	Ile	Ser	Leu	Leu	Gln	Ala	Gln	Val	Ser	Asn	260	265	270
Phe	Gln	Arg	Glu	Asn	Glu	Ala	Leu	Arg	Cys	Gly	Gln	Gly	Ala	Ser	275	280	285
Leu	Thr	Val	Val	Lys	Gln	Asn	Ala	Asp	Val	Ala	Leu	Gln	Asn	Leu	290	295	300
Arg	Val	Val	Met	Asn	Ser	Ala	Gln	Ala	Ser	Ile	Lys	Gln	Leu	Val	305	310	315
Ser	Gly	Ala	Glu	Thr	Leu	Asn	Leu	Val	Ala	Glu	Ile	Leu	Lys	Ser	320	325	330
Ile	Asp	Arg	Ile	Ser	Glu	Val	Lys	Asp	Glu	Glu	Glu	Asp	Ser		335	340	345
				350					355								

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARNOT03
- (B) CLONE: 2061561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46 :

Met	Gly	Gly	Lys	Pro	His	Lys	Glu	Pro	Arg	Ala	Lys	Gly	Pro	Leu	5	10	15
Ser	Ile	Phe	Tyr	Pro	Gly	Ser	Thr	Ala	Pro	Val	Ile	Thr	Gln	Arg	20	25	30
Thr	Pro	Xaa	Ala	Ala	Leu	Lys	Pro	Pro	Pro	Ile	Lys	Gly	Ala	Gly	35	40	45

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Pro	Thr	Ile	Ala	Pro	Ile	Lys	Gly	Xaa	Xaa	Asn	Phe	Gly	Lys	Arg
				50					55					60
Pro	Thr	Val	Thr	Xaa	Pro	Xaa	Trp	Xaa	Ile	Ser	Pro	Asn	Trp	Gly
				65					70					75
Lys	Arg	Gly	Xaa	Cys	Xaa	Xaa	Xaa	Gly	Ile	Lys	Trp	Val	Xaa	Pro
				80					85					90
Arg	Val	Ser	Gln	Ala	Arg	Thr	Phe	Lys	Thr	Thr	Ala	Asn	Glu	Leu
				95					100					105
Xaa	Phe	Xaa	Asp	Thr	Phe	Glu	Glu	Xaa	Xaa	Arg	Xaa	Xaa	His	Ala
				110					115					120
Xaa	Val	Ser	Xaa	Glu	Pro	Gln	Pro	Arg	Cys	Pro	Leu	Gly	Glu	Ser
				125					130					135
Arg	Ser	Leu	Gly	Ala	Ala	Val	Cys	Arg	Trp	Asp	Ser	Phe	Asp	Phe
				140					145					150

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PANCNOT04
- (B) CLONE: 2084489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47 :

Met	Pro	Pro	Val	Ser	Arg	Ser	Ser	Tyr	Ser	Glu	Asp	Ile	Val	Gly
				5					10					15
Ser	Arg	Arg	Arg	Arg	Arg	Ser	Ser	Ser	Gly	Ser	Pro	Pro	Ser	Pro
				20					25					30
Gln	Ser	Arg	Cys	Ser	Ser	Trp	Asp	Gly	Cys	Ser	Arg	Ser	His	Ser
				35					40					45
Arg	Gly	Arg	Glu	Gly	Leu	Arg	Pro	Pro	Trp	Ser	Glu	Leu	Asp	Val
				50					55					60
Gly	Ala	Leu	Tyr	Pro	Phe	Ser	Arg	Ser	Gly	Ser	Arg	Gly	Arg	Leu
				65					70					75
Pro	Arg	Phe	Arg	Asn	Tyr	Ala	Phe	Ala	Ser	Ser	Trp	Ser	Thr	Ser
				80					85					90
Tyr	Ser	Gly	Tyr	Arg	Tyr	His	Arg	His	Cys	Tyr	Ala	Glu	Glu	Arg
				95					100					105
Gln	Ser	Ala	Glu	Asp	Tyr	Glu	Lys	Glu	Glu	Ser	His	Arg	Gln	Arg
				110					115					120
Arg	Leu	Lys	Glu	Arg	Glu	Arg	Ile	Gly	Glu	Leu	Gly	Ala	Pro	Glu
				125					130					135
Val	Trp	Gly	Pro	Ser	Pro	Lys	Phe	Pro	Gln	Leu	Asp	Ser	Asp	Glu
				140					145					150
His	Thr	Pro	Val	Glu	Asp	Glu	Glu	Glu	Val	Thr	His	Gln	Lys	Ser
				155					160					165
Ser	Ser	Ser	Asp	Ser	Asn	Ser	Glu	Glu	His	Arg	Lys	Lys	Lys	Thr
				170					175					180
Ser	Arg	Ser	Arg	Asn	Lys	Lys	Lys	Arg	Lys	Asn	Lys	Ser	Ser	Lys
				185					190					195
Arg	Lys	His	Arg	Lys	Tyr	Ser	Asp	Ser	Asp	Ser	Asn	Ser	Glu	Ser

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Asp Thr Asn Ser	200	Asp Ser Asp Asp Asp	205	Lys Lys Arg Val Lys	210
Lys Lys Lys Lys	215	Lys Lys Lys His	220	Thr Lys Lys Lys	225
Asn Lys Lys Thr	230	Lys Lys Glu Ser Ser	235	Asp Ser Ser Cys Lys	240
Ser Glu Glu Asp	245	Leu Ser Glu Ala Thr	250	Trp Met Glu Gln Pro	255
Val Ala Asp Thr	260	Met Asp Leu Ile Gly	265	Pro Glu Ala Pro Ile	270
His Thr Ser Gln	275	Asp Glu Lys Pro Leu	280	Lys Tyr Gly His Ala	285
Leu Pro Gly Glu	290	Gly Ala Ala Met Ala	295	Glu Tyr Val Lys Ala	300
Lys Arg Ile Pro	305	Arg Arg Gly Glu Ile	310	Gly Leu Thr Ser Glu	315
Ile Gly Ser Phe	320	Glu Cys Ser Gly Tyr	325	Val Met Ser Gly Ser	330
His Arg Arg Met	335	Glu Ala Val Arg Leu	340	Arg Lys Glu Asn Gln	345
Tyr Ser Ala Asp	350	Glu Lys Arg Ala Leu	355	Ala Ser Phe Asn Gln	360
Glu Arg Arg Lys	365	Arg Glu Ser Lys Ile	370	Leu Ala Ser Phe Arg	375
Met Val His Lys	380	Lys Thr Lys Glu Lys	385	Asp Asp Lys	390
	395		400		

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SPLNFET02
- (B) CLONE: 2203226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48 :

Met His Pro Ala Gly	5	Leu Ala Ala Ala	10	Ala Ala Gly Thr Pro Arg	15
Leu Pro Ser Lys Arg	20	Arg Ile Pro Val	25	Ser Gln Pro Gly Met Ala	30
Asp Pro His Gln Leu	35	Phe Asp Asp Thr	40	Ser Ser Ala Gln Ser Arg	45
Gly Tyr Gly Ala Gln	50	Arg Ala Pro Gly	55	Gly Leu Ser Tyr Pro Ala	60
Ala Ser Pro Thr Pro	65	His Ala Ala Phe	70	Leu Ala Asp Pro Val Ser	75
Asn Met Ala Met Ala	80	Tyr Gly Ser Ser	85	Leu Ala Ala Gln Gly Lys	90
Glu Leu Val Asp Lys	95	Asn Ile Asp Arg	100	Phe Ile Pro Ile Thr Lys	105
Leu Lys Tyr Tyr Phe	110	Ala Val Asp Thr	115	Met Tyr Val Gly Arg Lys	120

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Leu	Gly	Leu	Leu	Phe	Phe	Pro	Tyr	Leu	His	Gln	Asp	Trp	Glu	Val	
				125					130					135	
Gln	Tyr	Gln	Gln	Asp	Thr	Pro	Val	Ala	Pro	Arg	Phe	Asp	Val	Asn	
				140					145					150	
Ala	Pro	Asp	Leu	Tyr	Ile	Pro	Ala	Met	Ala	Phe	Ile	Thr	Tyr	Val	
				155					160					165	
Leu	Val	Ala	Gly	Leu	Ala	Leu	Gly	Thr	Gln	Asp	Arg	Phe	Ser	Pro	
				170					175					180	
Asp	Leu	Leu	Gly	Leu	Gln	Ala	Ser	Ser	Ala	Leu	Ala	Trp	Leu	Thr	
				185					190					195	
Leu	Glu	Val	Leu	Ala	Ile	Leu	Leu	Ser	Leu	Tyr	Leu	Val	Thr	Val	
				200					205					210	
Asn	Thr	Asp	Leu	Thr	Thr	Ile	Asp	Leu	Val	Ala	Phe	Leu	Gly	Tyr	
				215					220					225	
Lys	Tyr	Val	Gly	Met	Ile	Gly	Gly	Val	Leu	Met	Gly	Leu	Leu	Phe	
				230					235					240	
Gly	Lys	Ile	Gly	Tyr	Tyr	Leu	Val	Leu	Gly	Trp	Cys	Cys	Val	Ala	
				245					250					255	
Ile	Phe	Val	Phe	Met	Ile	Arg	Thr	Leu	Arg	Leu	Lys	Ile	Leu	Ala	
				260					265					270	
Asp	Ala	Ala	Ala	Glu	Gly	Val	Pro	Val	Arg	Gly	Ala	Arg	Asn	Gln	
				275					280					285	
Leu	Arg	Met	Tyr	Leu	Thr	Met	Ala	Val	Ala	Ala	Ala	Gln	Pro	Met	
				290					295					300	
Leu	Met	Tyr	Trp	Leu	Thr	Phe	His	Leu	Val	Arg					
				305					310						

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT16
- (B) CLONE: 2232884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49 :

Met	Ala	Ser	Ala	Asp	Glu	Leu	Thr	Phe	His	Glu	Phe	Glu	Glu	Ala	
				5					10					15	
Thr	Asn	Leu	Leu	Ala	Asp	Thr	Pro	Asp	Ala	Ala	Thr	Thr	Ser	Arg	
				20					25					30	
Ser	Asp	Gln	Leu	Thr	Pro	Gln	Gly	His	Val	Ala	Val	Ala	Val	Gly	
				35					40					45	
Ser	Gly	Gly	Ser	Tyr	Gly	Ala	Glu	Asp	Glu	Val	Glu	Glu	Glu	Ser	
				50					55					60	
Asp	Lys	Ala	Ala	Leu	Leu	Gln	Glu	Gln	Gln	Gln	Gln	Gln	Gln	Pro	
				65					70					75	
Gly	Phe	Trp	Thr	Phe	Ser	Tyr	Tyr	Gln	Ser	Phe	Phe	Asp	Val	Asp	
				80					85					90	
Thr	Ser	Gln	Val	Leu	Asp	Arg	Ile	Lys	Gly	Ser	Leu	Leu	Pro	Arg	
				95					100					105	
Pro	Gly	His	Asn	Phe	Val	Arg	His	His	Leu	Arg	Asn	Arg	Pro	Asp	
				110					115					120	
Leu	Tyr	Gly	Pro	Phe	Trp	Ile	Cys	Ala	Thr	Leu	Ala	Phe	Val	Leu	

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Ala Val Thr Gly	125	Asn Leu Thr Leu Val	130	Leu Ala Gln Arg Arg	135
Pro Ser Ile His	140	Tyr Ser Pro Gln Phe	145	His Lys Val Thr Val	150
Gly Ile Ser Ile	155	Tyr Cys Tyr Ala Trp	160	Leu Val Pro Leu Ala	165
Trp Gly Phe Leu	170	Arg Trp Arg Lys Gly	175	Val Gln Glu Arg Met	180
Pro Tyr Thr Phe	185	Leu Glu Thr Val Cys	190	Ile Tyr Gly Tyr Ser	195
Phe Val Phe Ile	200	Pro Met Val Val Leu	205	Trp Leu Ile Pro Val	210
Trp Leu Gln Trp	215	Leu Phe Gly Ala Leu	220	Ala Leu Gly Leu Ser	225
Ala Gly Leu Val	230	Phe Thr Leu Trp Pro	235	Val Val Arg Glu Asp	240
Arg Leu Val Ala	245	Thr Val Leu Leu Ser	250	Val Val Val Leu Leu	255
Ala Leu Leu Ala	260	Met Gly Cys Lys Leu	265	Tyr Phe Phe Gln Ser	270
Pro Pro Glu Asn	275	Val Ala Pro Pro Pro	280	Gln Ile Thr Ser Leu	285
Ser Asn Ile Ala	290	Leu Ser Pro Thr Leu	295	Pro Gln Ser Leu Ala	300
Ser	305		310		315

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT11
- (B) CLONE: 2328134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50 :

Met Thr Pro Arg Thr	5	Trp Trp Pro Arg	10	Pro Ala Gly Trp Gly Thr	15
Cys Arg Ala Ala Gly	20	Trp Pro Arg Ser	25	Val Pro Trp Ala Arg Thr	30
Ala Ala Ser Leu Val	35	Phe Val Pro Thr	40	Arg Arg Arg Ser Gly Pro	45
Ser Gly Thr Ala Ser	50	Val Ala Ala Met	55	Ala Tyr His Ser Gly Tyr	60
Gly Ala His Gly Ser	65	Lys His Arg Ala	70	Arg Ala Ala Pro Asp Pro	75
Pro Pro Leu Phe Asp	80	Asp Thr Ser Gly	85	Gly Tyr Ser Ser Gln Pro	90
Gly Gly Tyr Pro Ala	95	Thr Gly Ala Asp	100	Val Ala Phe Ser Val Asn	105
His Leu Leu Gly Asp	110	Pro Met Ala Asn	115	Val Ala Met Ala Tyr Gly	120
Ser Ser Ile Ala Ser	125	His Gly Lys Asp	130	Met Val His Lys Glu Leu	135

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His	Arg	Phe	Val	Ser	Val	Ser	Lys	Leu	Lys	Tyr	Phe	Phe	Ala	Val
				140					145					150
Asp	Thr	Ala	Tyr	Val	Ala	Lys	Lys	Leu	Gly	Leu	Leu	Val	Phe	Pro
				155					160					165
Tyr	Thr	His	Gln	Asn	Trp	Glu	Val	Gln	Tyr	Ser	Arg	Asp	Ala	Pro
				170					175					180
Leu	Pro	Pro	Arg	Gln	Asp	Leu	Asn	Ala	Pro	Asp	Leu	Tyr	Ile	Pro
				185					190					195
Thr	Met	Ala	Phe	Ile	Thr	Tyr	Val	Leu	Leu	Ala	Gly	Met	Ala	Leu
				200					205					210
Gly	Ile	Gln	Lys	Arg	Phe	Ser	Pro	Glu	Val	Leu	Gly	Leu	Cys	Ala
				215					220					225
Ser	Thr	Ala	Leu	Val	Trp	Val	Val	Met	Glu	Val	Leu	Ala	Leu	Leu
				230					235					240
Leu	Gly	Leu	Tyr	Leu	Ala	Thr	Val	Arg	Ser	Asp	Leu	Ser	Thr	Phe
				245					250					255
His	Leu	Leu	Ala	Tyr	Ser	Gly	Tyr	Lys	Tyr	Val	Gly	Met	Ile	Leu
				260					265					270
Ser	Val	Leu	Thr	Gly	Leu	Leu	Phe	Gly	Ser	Asp	Gly	Tyr	Tyr	Val
				275					280					285
Ala	Leu	Ala	Trp	Thr	Ser	Ser	Ala	Leu	Met	Tyr	Phe	Ile	Val	Arg
				290					295					300
Ser	Leu	Arg	Thr	Ala	Ala	Leu	Gly	Pro	Asp	Ser	Met	Gly	Gly	Pro
				305					310					315
Val	Pro	Arg	Gln	Arg	Leu	Gln	Leu	Tyr	Leu	Thr	Leu	Gly	Ala	Ala
				320					325					330
Ala	Phe	Gln	Pro	Leu	Ile	Ile	Tyr	Trp	Leu	Thr	Phe	His	Leu	Val
				335					340					345

Arg

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ISLTNOT01
- (B) CLONE: 2382718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51 :

Met	Gly	Thr	Lys	Ala	Gln	Val	Glu	Arg	Lys	Leu	Leu	Cys	Leu	Phe
				5					10					15
Ile	Leu	Ala	Ile	Leu	Leu	Cys	Ser	Leu	Ala	Leu	Gly	Ser	Val	Thr
				20					25					30
Val	His	Ser	Ser	Glu	Pro	Glu	Val	Arg	Ile	Pro	Glu	Asn	Asn	Pro
				35					40					45
Val	Lys	Leu	Ser	Cys	Ala	Tyr	Ser	Gly	Phe	Ser	Ser	Pro	Arg	Val
				50					55					60
Glu	Trp	Lys	Phe	Asp	Gln	Gly	Asp	Thr	Thr	Arg	Leu	Val	Cys	Tyr
				65					70					75
Asn	Asn	Lys	Ile	Thr	Ala	Ser	Tyr	Glu	Asp	Arg	Val	Thr	Phe	Leu
				80					85					90
Pro	Thr	Gly	Ile	Thr	Phe	Lys	Ser	Val	Thr	Arg	Glu	Asp	Thr	Gly
				95					100					105
Thr	Tyr	Thr	Cys	Met	Val	Ser	Glu	Glu	Gly	Gly	Asn	Ser	Tyr	Gly

Glu Val Lys Val	110	Lys Leu Ile Val Leu	115	Val Pro Pro Ser Lys	120
Thr Val Asn Ile	125	Pro Ser Ser Ala Thr	130	Ile Gly Asn Arg Ala	135
Leu Thr Cys Ser	140	Glu Gln Asp Gly Ser	145	Pro Pro Ser Glu Tyr	150
Trp Phe Lys Asp	155	Gly Ile Val Met Pro	160	Thr Asn Pro Lys Ser	165
Arg Ala Phe Ser	170	Asn Ser Ser Tyr Val	175	Leu Asn Pro Thr Thr	180
Glu Leu Val Phe	185	Asp Pro Leu Ser Ala	190	Ser Asp Thr Gly Glu	195
Ser Cys Glu Ala	200	Arg Asn Gly Tyr Gly	205	Thr Pro Met Thr Ser	210
Ala Val Arg Met	215	Glu Ala Val Glu Arg	220	Val Gly Val Ile Val	225
Ala Ala Val Leu	230	Val Thr Leu Ile Leu	235	Leu Gly Ile Leu Val	240
Gly Ile Trp Phe	245	Ala Tyr Ser Arg Gly	250	His Phe Asp Arg Thr	255
Lys Gly Thr Ser	260	Ser Lys Lys Val Ile	265	Tyr Ser Gln Pro Ser	270
Arg Ser Glu Gly	275	Glu Phe Lys Gln Thr	280	Ser Ser Phe Leu Val	285
	290		295		

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ENDANOT01
- (B) CLONE: 2452208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52 :

Met Ala Ser Thr Gly	5	Ser Gln Ala Ser Asp	10	Ile Asp Glu Ile Phe	15
Gly Phe Phe Asn Asp	20	Gly Glu Pro Pro Thr	25	Lys Lys Pro Arg Lys	30
Leu Leu Pro Ser Leu	35	Lys Thr Lys Lys Pro	40	Arg Glu Leu Val Leu	45
Val Ile Gly Thr Gly	50	Ile Ser Ala Ala Val	55	Ala Pro Gln Val Pro	60
Ala Leu Lys Ser Trp	65	Lys Gly Leu Ile Gln	70	Ala Leu Leu Asp Ala	75
Ala Ile Asp Phe Asp	80	Leu Leu Glu Asp Glu	85	Glu Ser Lys Lys Phe	90
Gln Lys Cys Leu His	95	Glu Asp Lys Asn Leu	100	Val His Val Ala His	105
Asp Leu Ile Gln Lys	110	Leu Ser Pro Arg Thr	115	Ser Asn Val Arg Ser	120
Thr Phe Phe Lys Asp	125	Cys Leu Tyr Glu Val	130	Phe Asp Asp Leu Glu	135



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Ser	Lys	Met	Glu	Asp	Ser	Gly	Lys	Gln	Leu	Leu	Gln	Ser	Val	Leu	
				140					145					150	
His	Leu	Met	Glu	Asn	Gly	Ala	Leu	Val	Leu	Thr	Thr	Asn	Phe	Asp	
				155					160					165	
Asn	Leu	Leu	Glu	Leu	Tyr	Ala	Ala	Asp	Gln	Gly	Lys	Gln	Leu	Glu	
				170					175					180	
Ser	Leu	Asp	Leu	Thr	Asp	Glu	Lys	Lys	Val	Leu	Glu	Trp	Ala	Gln	
				185					190					195	
Glu	Lys	Arg	Lys	Leu	Ser	Val	Leu	His	Ile	His	Gly	Val	Tyr	Thr	
				200					205					210	
Asn	Pro	Ser	Gly	Ile	Val	Leu	His	Pro	Ala	Gly	Tyr	Gln	Asn	Val	
				215					220					225	
Leu	Arg	Asn	Thr	Glu	Val	Met	Arg	Glu	Ile	Gln	Lys	Leu	Tyr	Glu	
				230					235					240	
Asn	Lys	Ser	Phe	Leu	Phe	Leu	Gly	Cys	Gly	Trp	Thr	Val	Asp	Asp	
				245					250					255	
Thr	Thr	Phe	Gln	Ala	Leu	Phe	Leu	Glu	Ala	Val	Lys	His	Lys	Ser	
				260					265					270	
Asp	Leu	Glu	His	Phe	Met	Leu	Val	Arg	Arg	Gly	Asp	Val	Asp	Glu	
				275					280					285	
Phe	Lys	Lys	Leu	Arg	Glu	Asn	Met	Leu	Asp	Lys	Gly	Ile	Lys	Val	
				290					295					300	
Ile	Ser	Tyr	Gly	Asp	Asp	Tyr	Ala	Asp	Leu	Pro	Glu	Tyr	Phe	Lys	
				305					310					315	
Arg	Leu	Thr	Cys	Glu	Ile	Ser	Thr	Arg	Gly	Thr	Ser	Ala	Gly	Met	
				320					325					330	
Val	Arg	Glu	Gly	Gln	Leu	Asn	Gly	Ser	Ser	Ala	Ala	His	Ser	Glu	
				335					340					345	
Ile	Arg	Gly	Cys	Ser	Thr										
				350											

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ENDANOT01
- (B) CLONE: 2457825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53 :

Met	Thr	Ala	Lys	Lys	Gln	Cys	Leu	Leu	Arg	Leu	Gly	Val	Leu	Arg	
				5					10					15	
Gln	Asp	Trp	Pro	Asp	Thr	Asn	Arg	Leu	Leu	Gly	Ser	Ala	Asn	Val	
				20					25					30	
Val	Pro	Glu	Ala	Leu	Gln	Arg	Phe	Thr	Arg	Ala	Ala	Ala	Asp	Phe	
				35					40					45	
Ala	Thr	His	Gly	Lys	Leu	Gly	Lys	Leu	Glu	Phe	Ala	Gln	Asp	Ala	
				50					55					60	
His	Gly	Gln	Pro	Asp	Val	Ser	Ala	Phe	Asp	Phe	Thr	Ser	Met	Met	
				65					70					75	
Arg	Ala	Glu	Ser	Ser	Ala	Arg	Val	Gln	Glu	Lys	His	Gly	Ala	Arg	
				80					85					90	
Leu	Leu	Leu	Gly	Leu	Val	Gly	Asp	Cys	Leu	Val	Glu	Pro	Phe	Trp	

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Pro	Leu	Gly	Thr	95	Gly	Val	Ala	Arg	Gly	100	Phe	Leu	Ala	Ala	Phe	Asp	105
				110						115							120
Ala	Ala	Trp	Met	125	Val	Lys	Arg	Trp	Ala	130	Glu	Gly	Ala	Glu	Ser	Leu	135
Glu	Val	Leu	Ala	140	Glu	Arg	Glu	Ser	Leu	145	Tyr	Gln	Leu	Leu	Ser	Gln	150
Thr	Ser	Pro	Glu	155	Asn	Met	His	Arg	Asn	160	Val	Ala	Gln	Tyr	Gly	Leu	165
Asp	Pro	Ala	Thr	170	Arg	Tyr	Pro	Asn	Leu	175	Asn	Leu	Arg	Ala	Val	Thr	180
Pro	Asn	Gln	Val	185	Arg	Asp	Leu	Tyr	Asp	190	Val	Leu	Ala	Lys	Glu	Pro	195
Val	Gln	Arg	Asp	200	Asn	Asp	Lys	Thr	Asp	205	Thr	Gly	Met	Pro	Ala	Thr	210
Gly	Ser	Ala	Gly	215	Thr	Gln	Glu	Glu	Leu	220	Leu	Arg	Trp	Cys	Gln	Glu	225
Gln	Thr	Ala	Gly	230	Tyr	Pro	Gly	Val	His	235	Val	Ser	Asp	Leu	Ser	Ser	240
Ser	Trp	Ala	Asp	245	Gly	Leu	Ala	Leu	Cys	250	Ala	Leu	Val	Tyr	Arg	Leu	255
Gln	Pro	Gly	Leu	260	Leu	Glu	Pro	Ser	Glu	265	Leu	Gln	Gly	Leu	Gly	Ala	270
Leu	Glu	Ala	Thr	275	Ala	Trp	Ala	Leu	Lys	280	Val	Ala	Glu	Asn	Glu	Leu	285
Gly	Ile	Thr	Pro	290	Val	Val	Ser	Ala	Gln	295	Ala	Val	Val	Ala	Gly	Ser	300
Asp	Pro	Leu	Gly	305	Leu	Ile	Ala	Tyr	Leu	310	Ser	His	Phe	His	Ser	Ala	315
Phe	Lys	Ser	Met	320	Ala	His	Ser	Pro	Gly	325	Pro	Val	Ser	Gln	Ala	Ser	330
Pro	Gly	Thr	Ser	335	Ser	Ala	Val	Leu	Phe	340	Leu	Ser	Lys	Leu	Gln	Arg	345
Thr	Leu	Gln	Arg	350	Ser	Arg	Ala	Lys	Glu	355	Asn	Ala	Glu	Asp	Ala	Gly	360
Gly	Lys	Lys	Leu	365	Arg	Leu	Glu	Met	Glu	370	Ala	Glu	Thr	Pro	Ser	Thr	375
Glu	Val	Pro	Pro	380	Asp	Pro	Glu	Pro	Gly	385	Val	Pro	Leu	Thr	Pro	Pro	390
Ser	Gln	His	Gln	395	Glu	Ala	Gly	Ala	Gly	400	Asp	Leu	Cys	Ala	Leu	Cys	405
Gly	Glu	His	Leu	410	Tyr	Val	Leu	Glu	Arg	415	Leu	Cys	Val	Asn	Gly	His	420
Phe	Phe	His	Arg	425	Ser	Cys	Phe	Arg	Cys	430	His	Thr	Cys	Glu	Ala	Thr	435
Leu	Trp	Pro	Gly	440	Gly	Tyr	Glu	Gln	His	445	Pro	Gly	Ser	Arg	Thr	Ser	450
Gln	Phe	Phe	Phe	455	Ser	Ala	Leu	Val	Ala	460	Met	Glu	Lys	Glu	Glu	Lys	465
Glu	Ser	Pro	Phe	470	Ser	Ser	Glu	Glu	Glu	475	Glu	Glu	Asp	Val	Pro	Leu	480
Asp	Ser	Asp	Val	485	Glu	Gln	Ala	Leu	Gln	490	Thr	Phe	Ala	Lys	Thr	Ser	495
Gly	Thr	Met	Asn	500	Asn	Tyr	Pro	Thr	Trp	505	Arg	Arg	Thr	Leu	Leu	Arg	510
Arg	Ala	Lys	Glu	515	Glu	Glu	Met	Lys	Arg	520	Phe	Cys	Lys	Ala	Gln	Thr	525
Ile	Gln	Arg	Arg	530	Leu	Asn	Glu	Ile	Glu	535	Ala	Ala	Leu	Arg	Glu	Leu	540
Glu	Ala	Glu	Gly	545	Val	Lys	Leu	Glu	Leu	550	Ala	Leu	Arg	Arg	Gln	Ser	555

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Ser	Ser	Pro	Glu	Gln	Gln	Lys	Lys	Leu	Trp	Val	Gly	Gln	Leu	Leu
				560					565					570
Gln	Leu	Val	Asp	Lys	Lys	Asn	Ser	Leu	Val	Ala	Glu	Glu	Ala	Glu
				575					580					585
Leu	Met	Ile	Thr	Val	Gln	Glu	Leu	Asn	Leu	Glu	Glu	Lys	Gln	Trp
				590					595					600
Gln	Leu	Asp	Gln	Glu	Leu	Arg	Gly	Tyr	Met	Asn	Arg	Glu	Glu	Asn
				605					610					615
Leu	Lys	Thr	Ala	Ala	Asp	Arg	Gln	Ala	Glu	Asp	Gln	Val	Leu	Arg
				620					625					630
Lys	Leu	Val	Asp	Leu	Val	Asn	Gln	Arg	Asp	Ala	Leu	Ile	Arg	Phe
				635					640					645
Gln	Glu	Glu	Arg	Arg	Leu	Ser	Glu	Leu	Ala	Leu	Gly	Thr	Gly	Ala
				650					655					660
Gln	Gly													

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1NOT03
- (B) CLONE: 2470740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54 :

Met	Ala	Ser	Trp	Pro	Ala	Ser	Pro	Leu	Gln	Trp	Gly	Pro	Pro	Leu
				5					10					15
Ala	Ser	Cys	Pro	Ser	Cys	Cys	Cys	Cys	Cys	Phe	His	Cys	Trp	Gln
				20					25					30
Pro	Arg	Val	Gly	Val	Ala	Cys	Arg	Gln	Arg	Cys	Trp	Pro	Leu	Arg
				35					40					45
Trp	Gly	Trp	Trp	Val	Trp	Gly	Pro	Pro	Thr	Cys	Ser	Phe	Val	Gln
				50					55					60
Pro	Cys	Thr	Cys	Pro	Pro	Val	Phe	Ser	Tyr	Ser	Trp	Pro	Arg	Val
				65					70					75
Pro	His	Trp	Gly	Pro	Ser	Trp	Xaa	Met	Ser	Trp	Arg	Arg	Arg	Leu
				80					85					90
Met	Gly	Val	Pro	Leu	Gly	Leu	Trp	Asn	Cys	Leu	Val	Leu	Lys	Leu
				95					100					105
Xaa	Gln	Gly	Leu	Ala	Pro	Thr	Ser	Gly	Gly					
				110					115					

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

PF-0459 US

(A) LIBRARY: SMCANOT01

(B) CLONE: 2479092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55 :

Met	Glu	Ala	Leu	Arg	Arg	Ala	His	Glu	Val	Ala	Leu	Arg	Leu	Leu	
			5						10						15
Leu	Cys	Arg	Pro	Trp	Ala	Ser	Arg	Ala	Ala	Ala	Arg	Pro	Lys	Pro	
			20						25						30
Ser	Ala	Ser	Glu	Val	Leu	Thr	Arg	His	Leu	Leu	Gln	Arg	Arg	Leu	
			35						40						45
Pro	His	Trp	Thr	Ser	Phe	Cys	Val	Pro	Tyr	Ser	Ala	Val	Arg	Asn	
			50						55						60
Asp	Gln	Phe	Gly	Leu	Ser	His	Phe	Asn	Trp	Pro	Val	Gln	Gly	Ala	
			65						70						75
Asn	Tyr	His	Val	Leu	Arg	Thr	Gly	Cys	Phe	Pro	Phe	Ile	Lys	Tyr	
			80						85						90
His	Cys	Ser	Lys	Ala	Pro	Trp	Gln	Asp	Leu	Ala	Arg	Gln	Asn	Arg	
			95						100						105
Phe	Phe	Thr	Ala	Leu	Lys	Val	Val	Asn	Leu	Gly	Ile	Pro	Thr	Leu	
			110						115						120
Leu	Tyr	Gly	Leu	Gly	Ser	Trp	Leu	Phe	Ala	Arg	Val	Thr	Glu	Thr	
			125						130						135
Val	His	Thr	Ser	Tyr	Gly	Pro	Ile	Thr	Val	Tyr	Phe	Leu	Asn	Lys	
			140						145						150
Glu	Asp	Glu	Gly	Ala	Met	Tyr									
			155												

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: SMCANOT01

(B) CLONE: 2480544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56 :

Met	Pro	Pro	Ala	Gly	Leu	Arg	Arg	Ala	Ala	Pro	Leu	Thr	Ala	Ile	
			5						10						15
Ala	Leu	Leu	Val	Leu	Gly	Ala	Pro	Leu	Val	Leu	Ala	Gly	Glu	Asp	
			20						25						30
Cys	Leu	Trp	Tyr	Leu	Asp	Arg	Asn	Gly	Ser	Trp	His	Pro	Gly	Phe	
			35						40						45
Asn	Cys	Glu	Phe	Phe	Thr	Phe	Cys	Cys	Gly	Thr	Cys	Tyr	His	Arg	
			50						55						60
Tyr	Cys	Cys	Arg	Asp	Leu	Thr	Leu	Leu	Ile	Thr	Glu	Arg	Gln	Gln	
			65						70						75
Lys	His	Cys	Leu	Ala	Phe	Ser	Pro	Lys	Thr	Ile	Ala	Gly	Ile	Ala	
			80						85						90
Ser	Ala	Val	Ile	Leu	Phe	Val	Ala	Val	Val	Ala	Thr	Thr	Ile	Cys	
			95						100						105
Cys	Phe	Leu	Cys	Ser	Cys	Cys	Tyr	Leu	Tyr	Arg	Arg	Arg	Gln	Gln	
			110						115						120

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Leu	Gln	Ser	Pro	Phe	Glu	Gly	Gln	Glu	Ile	Pro	Met	Thr	Gly	Ile
				125					130					135
Pro	Val	Gln	Pro	Val	Tyr	Pro	Tyr	Pro	Gln	Asp	Pro	Lys	Ala	Gly
				140					145					150
Pro	Ala	Pro	Pro	Gln	Pro	Gly	Phe	Met	Tyr	Pro	Pro	Ser	Gly	Pro
				155					160					165
Ala	Pro	Gln	Tyr	Pro	Leu	Tyr	Pro	Ala	Gly	Pro	Pro	Val	Tyr	Asn
				170					175					180
Pro	Ala	Ala	Pro	Pro	Pro	Tyr	Met	Pro	Pro	Gln	Pro	Ser	Tyr	Pro
				185					190					195
Gly	Ala													

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT21
- (B) CLONE: 2518547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57 :

Met	Gly	Gly	Ala	Ser	Arg	Arg	Val	Glu	Ser	Gly	Ala	Trp	Ala	Tyr
				5					10					15
Leu	Ser	Pro	Leu	Val	Leu	Arg	Lys	Glu	Leu	Glu	Ser	Leu	Val	Glu
				20					25					30
Asn	Glu	Gly	Ser	Glu	Val	Leu	Ala	Leu	Pro	Glu	Leu	Pro	Ser	Ala
				35					40					45
His	Pro	Ile	Ile	Phe	Trp	Asn	Leu	Leu	Trp	Tyr	Phe	Gln	Arg	Leu
				50					55					60
Arg	Leu	Pro	Ser	Ile	Leu	Pro	Gly	Leu	Val	Leu	Ala	Ser	Cys	Asp
				65					70					75
Gly	Pro	Ser	His	Ser	Gln	Ala	Pro	Ser	Pro	Trp	Leu	Thr	Pro	Asp
				80					85					90
Pro	Ala	Ser	Val	Gln	Val	Arg	Leu	Leu	Trp	Asp	Val	Leu	Thr	Pro
				95					100					105
Asp	Pro	Asn	Ser	Cys	Pro	Pro	Leu	Tyr	Val	Leu	Trp	Arg	Val	His
				110					115					120
Ser	Gln	Ile	Pro	Gln	Arg	Val	Val	Trp	Pro	Gly	Pro	Val	Pro	Ala
				125					130					135
Ser	Leu	Ser	Leu	Ala	Leu	Leu	Glu	Ser	Val	Leu	Arg	His	Val	Gly
				140					145					150
Leu	Asn	Glu	Val	His	Lys	Ala	Val	Gly	Leu	Leu	Leu	Glu	Thr	Leu
				155					160					165
Gly	Pro	Pro	Pro	Thr	Gly	Leu	His	Leu	Gln	Arg	Gly	Ile	Tyr	Arg
				170					175					180
Glu	Ile	Leu	Phe	Leu	Thr	Met	Ala	Ala	Leu	Gly	Lys	Asp	His	Val
				185					190					195
Asp	Ile	Val	Ala	Phe	Asp	Lys	Lys	Tyr	Lys	Ser	Ala	Phe	Asn	Lys
				200					205					210
Leu	Ala	Ser	Ser	Met	Gly	Lys	Glu	Glu	Leu	Arg	His	Arg	Arg	Ala
				215					220					225
Gln	Met	Pro	Thr	Pro	Lys	Ala	Ile	Asp	Cys	Arg	Lys	Cys	Phe	Gly
				230					235					240

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Ala Pro Pro Glu Cys  
245

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GBLANOT02
- (B) CLONE: 2530650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58 :

Met	Leu	Leu	Pro	Gln	Leu	Cys	Trp	Leu	Pro	Leu	Leu	Ala	Gly	Leu	
				5					10					15	
Leu	Pro	Pro	Val	Pro	Ala	Gln	Lys	Phe	Ser	Ala	Leu	Thr	Phe	Leu	
				20					25					30	
Arg	Val	Asp	Gln	Asp	Lys	Asp	Lys	Asp	Cys	Ser	Leu	Asp	Cys	Ala	
				35					40					45	
Gly	Ser	Pro	Gln	Lys	Pro	Leu	Cys	Ala	Ser	Asp	Gly	Arg	Thr	Phe	
				50					55					60	
Leu	Ser	Arg	Cys	Glu	Phe	Gln	Arg	Ala	Lys	Cys	Lys	Asp	Pro	Gln	
				65					70					75	
Leu	Glu	Ile	Ala	Tyr	Arg	Gly	Asn	Cys	Lys	Asp	Val	Ser	Arg	Cys	
				80					85					90	
Val	Ala	Glu	Arg	Lys	Tyr	Thr	Gln	Glu	Gln	Ala	Arg	Lys	Glu	Phe	
				95					100					105	
Gln	Gln	Val	Phe	Ile	Pro	Glu	Cys	Asn	Asp	Asp	Gly	Thr	Tyr	Ser	
				110					115					120	
Gln	Val	Gln	Cys	His	Ser	Tyr	Thr	Gly	Tyr	Cys	Trp	Cys	Val	Thr	
				125					130					135	
Pro	Asn	Gly	Arg	Pro	Ile	Ser	Gly	Thr	Ala	Val	Ala	His	Lys	Thr	
				140					145					150	
Pro	Arg	Cys	Pro	Gly	Ser	Val	Asn	Glu	Lys	Leu	Pro	Gln	Arg	Glu	
				155					160					165	
Gly	Thr	Gly	Lys	Thr	Asp	Asp	Ala	Ala	Ala	Pro	Ala	Leu	Glu	Thr	
				170					175					180	
Gln	Pro	Gln	Gly	Asp	Glu	Glu	Asp	Ile	Ala	Ser	Arg	Tyr	Pro	Thr	
				185					190					195	
Leu	Trp	Thr	Glu	Gln	Val	Lys	Ser	Arg	Gln	Asn	Lys	Thr	Asn	Lys	
				200					205					210	
Asn	Ser	Val	Ser	Ser	Cys	Asp	Gln	Glu	His	Gln	Ser	Ala	Leu	Glu	
				215					220					225	
Glu	Ala	Lys	Gln	Pro	Lys	Asn	Asp	Asn	Val	Val	Ile	Pro	Glu	Cys	
				230					235					240	
Ala	His	Gly	Gly	Leu	Tyr	Lys	Pro	Val	Gln	Cys	His	Pro	Ser	Thr	
				245					250					255	
Gly	Tyr	Cys	Trp	Cys	Val	Leu	Val	Asp	Thr	Gly	Arg	Pro	Ile	Pro	
				260					265					270	
Gly	Thr	Ser	Thr	Arg	Tyr	Glu	Gln	Pro	Lys	Cys	Asp	Asn	Thr	Gly	
				275					280					285	
Gln	Gly	Pro	Pro	Ser	Gln	Ser	Pro	Gly	Pro	Val	Gln	Gly	Pro	Pro	
				290					295					300	
Ala	Thr	Arg	Leu	Ser	Gly	Cys	Gln	Lys	Ala						

## (2) INFORMATION FOR SEQ ID NO: 59:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THYMNOT04
- (B) CLONE: 2652271

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59 :

Met	Arg	Pro	Ala	Ala	Leu	Arg	Gly	Ala	Leu	Leu	Gly	Cys	Leu	Cys	5	10	15
Leu	Ala	Leu	Leu	Cys	Leu	Gly	Gly	Ala	Asp	Lys	Arg	Leu	Arg	Asp	20	25	30
Asn	His	Glu	Trp	Lys	Lys	Leu	Ile	Met	Val	Gln	His	Trp	Pro	Glu	35	40	45
Thr	Val	Cys	Glu	Lys	Ile	Gln	Asn	Asp	Cys	Arg	Asp	Pro	Pro	Asp	50	55	60
Tyr	Trp	Thr	Ile	His	Gly	Leu	Trp	Pro	Asp	Lys	Ser	Glu	Gly	Cys	65	70	75
Asn	Arg	Ser	Trp	Pro	Phe	Asn	Leu	Glu	Glu	Ile	Lys	Asp	Leu	Leu	80	85	90
Pro	Glu	Met	Arg	Ala	Tyr	Trp	Pro	Asp	Val	Ile	His	Ser	Phe	Pro	95	100	105
Asn	Arg	Ser	Arg	Phe	Trp	Lys	His	Glu	Trp	Glu	Lys	His	Gly	Thr	110	115	120
Cys	Ala	Ala	Gln	Val	Asp	Ala	Leu	Asn	Ser	Gln	Lys	Lys	Tyr	Phe	125	130	135
Gly	Arg	Ser	Leu	Glu	Leu	Tyr	Arg	Glu	Leu	Asp	Leu	Asn	Ser	Val	140	145	150
Leu	Leu	Lys	Leu	Gly	Ile	Lys	Pro	Ser	Ile	Asn	Tyr	Tyr	Gln	Val	155	160	165
Ala	Asp	Phe	Lys	Asp	Ala	Leu	Ala	Arg	Val	Tyr	Gly	Val	Ile	Pro	170	175	180
Lys	Ile	Gln	Cys	Leu	Pro	Pro	Ser	Gln	Asp	Glu	Glu	Val	Gln	Thr	185	190	195
Ile	Gly	Gln	Ile	Glu	Leu	Cys	Leu	Thr	Lys	Gln	Asp	Gln	Gln	Leu	200	205	210
Gln	Asn	Cys	Thr	Glu	Pro	Gly	Glu	Gln	Pro	Ser	Pro	Lys	Gln	Glu	215	220	225
Val	Trp	Leu	Ala	Asn	Gly	Ala	Ala	Glu	Ser	Arg	Gly	Leu	Arg	Val	230	235	240
Cys	Glu	Asp	Gly	Pro	Val	Phe	Tyr	Pro	Pro	Pro	Lys	Lys	Thr	Lys	245	250	255

His

## (2) INFORMATION FOR SEQ ID NO: 60:

## (i) SEQUENCE CHARACTERISTICS:

PF-0459 US

(A) LENGTH: 160 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: LUNGTUT11  
(B) CLONE: 2746976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60 :

Met	Gln	Phe	Met	Leu	Leu	Phe	Ser	Arg	Gln	Gly	Lys	Leu	Arg	Leu	
				5					10					15	
Gln	Lys	Trp	Tyr	Val	Pro	Leu	Ser	Asp	Lys	Glu	Lys	Arg	Lys	Ile	
				20					25					30	
Thr	Arg	Glu	Leu	Val	Gln	Thr	Val	Leu	Ala	Arg	Lys	Pro	Lys	Met	
				35					40					45	
Cys	Ser	Phe	Leu	Glu	Trp	Arg	Asp	Leu	Lys	Ile	Val	Tyr	Lys	Arg	
				50					55					60	
Tyr	Ala	Ser	Leu	Tyr	Phe	Cys	Cys	Ala	Ile	Glu	Asp	Gln	Asp	Asn	
				65					70					75	
Glu	Leu	Ile	Thr	Leu	Glu	Ile	Ile	His	Arg	Tyr	Val	Glu	Leu	Leu	
				80					85					90	
Asp	Lys	Tyr	Phe	Gly	Ser	Val	Cys	Glu	Leu	Asp	Ile	Ile	Phe	Asn	
				95					100					105	
Phe	Glu	Lys	Ala	Tyr	Phe	Ile	Leu	Asp	Glu	Phe	Leu	Leu	Gly	Gly	
				110					115					120	
Glu	Val	Gln	Glu	Thr	Ser	Lys	Lys	Asn	Val	Leu	Lys	Ala	Ile	Glu	
				125					130					135	
Gln	Ala	Asp	Leu	Leu	Gln	Glu	Asp	Ala	Lys	Glu	Ala	Glu	Thr	Pro	
				140					145					150	
Arg	Ser	Val	Leu	Glu	Glu	Ile	Gly	Leu	Thr						
				155					160						

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: THP1AZS08  
(B) CLONE: 2753496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61 :

Met	Lys	Arg	Ala	Leu	Gly	Arg	Arg	Lys	Gly	Val	Trp	Leu	Arg	Leu	
				5					10					15	
Arg	Lys	Ile	Leu	Phe	Cys	Val	Leu	Gly	Leu	Tyr	Ile	Ala	Ile	Pro	
				20					25					30	
Phe	Leu	Ile	Lys	Leu	Cys	Pro	Gly	Ile	Gln	Ala	Lys	Leu	Ile	Phe	
				35					40					45	
Leu	Asn	Phe	Val	Arg	Val	Pro	Tyr	Phe	Ile	Asp	Leu	Lys	Lys	Pro	
				50					55					60	
Gln	Asp	Gln	Gly	Leu	Asn	His	Thr	Cys	Asn	Tyr	Tyr	Leu	Gln	Pro	
				65					70					75	
Glu	Glu	Asp	Val	Thr	Ile	Gly	Val	Trp	His	Thr	Val	Pro	Ala	Val	



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				80					85					90
Trp	Trp	Lys	Asn	Ala	Gln	Gly	Lys	Asp	Gln	Met	Trp	Tyr	Glu	Asp
				95					100					105
Ala	Leu	Ala	Ser	Ser	His	Pro	Ile	Ile	Leu	Tyr	Leu	His	Gly	Asn
				110					115					120
Ala	Gly	Thr	Arg	Gly	Gly	Asp	His	Arg	Val	Glu	Leu	Tyr	Lys	Val
				125					130					135
Leu	Ser	Ser	Leu	Gly	Tyr	His	Val	Val	Thr	Phe	Asp	Tyr	Arg	Gly
				140					145					150
Trp	Gly	Asp	Ser	Val	Gly	Thr	Pro	Ser	Glu	Arg	Gly	Met	Thr	Tyr
				155					160					165
Asp	Ala	Leu	His	Val	Phe	Asp	Trp	Ile	Lys	Ala	Arg	Ser	Gly	Asp
				170					175					180
Asn	Pro	Val	Tyr	Ile	Trp	Gly	His	Ser	Leu	Gly	Thr	Gly	Val	Ala
				185					190					195
Thr	Asn	Leu	Val	Arg	Arg	Leu	Cys	Glu	Arg	Glu	Thr	Pro	Pro	Asp
				200					205					210
Ala	Leu	Ile	Leu	Glu	Ser	Pro	Phe	Thr	Asn	Ile	Arg	Glu	Glu	Ala
				215					220					225
Lys	Ser	His	Pro	Phe	Ser	Val	Ile	Tyr	Arg	Tyr	Phe	Pro	Gly	Phe
				230					235					240
Asp	Trp	Phe	Phe	Leu	Asp	Pro	Ile	Thr	Ser	Ser	Gly	Ile	Lys	Phe
				245					250					255
Ala	Asn	Asp	Glu	Asn	Val	Lys	His	Ile	Ser	Cys	Pro	Leu	Leu	Ile
				260					265					270
Leu	His	Ala	Glu	Asp	Asp	Pro	Val	Val	Pro	Phe	Gln	Leu	Gly	Arg
				275					280					285
Lys	Leu	Tyr	Ser	Ile	Ala	Ala	Pro	Ala	Arg	Ser	Phe	Arg	Asp	Phe
				290					295					300
Lys	Val	Gln	Phe	Val	Pro	Phe	His	Ser	Asp	Leu	Gly	Tyr	Arg	His
				305					310					315
Lys	Tyr	Ile	Tyr	Lys	Ser	Pro	Glu	Leu	Pro	Arg	Ile	Leu	Arg	Glu
				320					325					330
Phe	Leu	Gly	Lys	Ser	Glu	Pro	Glu	His	Gln	His				
				335					340					

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARTUT03
- (B) CLONE: 2781553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62 :

Met	Ala	Glu	Gly	Glu	Asp	Val	Gly	Trp	Trp	Arg	Ser	Trp	Leu	Gln
				5					10					15
Gln	Ser	Tyr	Gln	Ala	Val	Lys	Glu	Lys	Ser	Ser	Glu	Ala	Leu	Glu
				20					25					30
Phe	Met	Lys	Arg	Asp	Leu	Thr	Glu	Phe	Thr	Gln	Val	Val	Gln	His
				35					40					45
Asp	Thr	Ala	Cys	Thr	Ile	Ala	Ala	Thr	Ala	Ser	Val	Val	Lys	Glu
				50					55					60

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Lys	Leu	Ala	Thr	Glu	Gly	Ser	Ser	Gly	Ala	Thr	Glu	Lys	Met	Lys
				65					70					75
Lys	Gly	Leu	Ser	Asp	Phe	Leu	Gly	Val	Ile	Ser	Asp	Thr	Phe	Ala
				80					85					90
Pro	Ser	Pro	Asp	Lys	Thr	Ile	Asp	Cys	Asp	Val	Ile	Thr	Leu	Met
				95					100					105
Gly	Thr	Pro	Ser	Gly	Thr	Ala	Glu	Pro	Tyr	Asp	Gly	Thr	Lys	Ala
				110					115					120
Arg	Leu	Tyr	Ser	Leu	Gln	Ser	Asp	Pro	Ala	Thr	Tyr	Cys	Asn	Glu
				125					130					135
Pro	Asp	Gly	Pro	Pro	Glu	Leu	Phe	Asp	Ala	Trp	Leu	Ser	Gln	Phe
				140					145					150
Cys	Leu	Glu	Glu	Lys	Lys	Gly	Glu	Ile	Ser	Glu	Leu	Leu	Val	Gly
				155					160					165
Ser	Pro	Ser	Ile	Arg	Ala	Leu	Tyr	Thr	Lys	Met	Val	Pro	Ala	Ala
				170					175					180
Val	Ser	His	Ser	Glu	Phe	Trp	His	Arg	Tyr	Phe	Tyr	Lys	Val	His
				185					190					195
Gln	Leu	Glu	Gln	Glu	Gln	Ala	Arg	Arg	Asp	Ala	Leu	Lys	Gln	Arg
				200					205					210
Ala	Glu	Gln	Ser	Ile	Ser	Glu	Glu	Pro	Gly	Trp	Glu	Glu	Glu	Glu
				215					220					225
Glu	Glu	Leu	Met	Gly	Ile	Ser	Pro	Ile	Ser	Pro	Lys	Glu	Ala	Lys
				230					235					240
Val	Pro	Val	Ala	Lys	Ile	Ser	Thr	Phe	Pro	Glu	Gly	Glu	Pro	Gly
				245					250					255
Pro	Gln	Ser	Pro	Cys	Glu	Glu	Asn	Leu	Val	Thr	Ser	Val	Glu	Pro
				260					265					270
Pro	Ala	Glu	Val	Thr	Pro	Ser	Glu	Ser	Ser	Glu	Ser	Ile	Ser	Leu
				275					280					285
Val	Thr	Gln	Ile	Ala	Asn	Pro	Ala	Thr	Ala	Pro	Glu	Ala	Arg	Val
				290					295					300
Leu	Pro	Lys	Asp	Leu	Ser	Gln	Lys	Leu	Leu	Glu	Ala	Ser	Leu	Glu
				305					310					315
Glu	Gln	Gly	Leu	Ala	Val	Asp	Val	Gly	Glu	Thr	Gly	Pro	Ser	Pro
				320					325					330
Pro	Ile	His	Ser	Lys	Pro	Leu	Thr	Pro	Ala	Gly	His	Thr	Gly	Gly
				335					340					345
Pro	Glu	Pro	Arg	Pro	Pro	Ala	Arg	Val	Glu	Thr	Leu	Arg	Glu	Glu
				350					355					360
Ala	Pro	Thr	Asp	Leu	Arg	Val	Phe	Glu	Leu	Asn	Ser	Asp	Ser	Gly
				365					370					375
Lys	Ser	Thr	Pro	Ser	Asn	Asn	Gly	Lys	Lys	Gly	Ser	Ser	Thr	Asp
				380					385					390
Ile	Ser	Glu	Asp	Trp	Glu	Lys	Asp	Phe	Asp	Leu	Asp	Met	Thr	Glu
				395					400					405
Glu	Glu	Val	Gln	Met	Ala	Leu	Ser	Lys	Val	Asp	Ala	Ser	Gly	Glu
				410					415					420
Leu	Glu	Asp	Val	Glu	Trp	Glu	Asp	Trp	Glu					
				425					430					

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ADRETUT06
- (B) CLONE: 2821925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63 :

Met	Gly	Pro	Val	Arg	Leu	Gly	Ile	Leu	Leu	Phe	Leu	Phe	Leu	Ala	
				5					10					15	
Val	His	Glu	Ala	Trp	Ala	Gly	Met	Leu	Lys	Glu	Glu	Asp	Asp	Asp	
				20					25					30	
Thr	Glu	Arg	Leu	Pro	Ser	Lys	Cys	Glu	Val	Cys	Lys	Leu	Leu	Ser	
				35					40					45	
Thr	Glu	Leu	Gln	Ala	Glu	Leu	Ser	Arg	Thr	Gly	Arg	Ser	Arg	Glu	
				50					55					60	
Val	Leu	Glu	Leu	Gly	Gln	Val	Leu	Asp	Thr	Gly	Lys	Arg	Lys	Arg	
				65					70					75	
His	Val	Pro	Tyr	Ser	Val	Ser	Glu	Thr	Arg	Leu	Glu	Glu	Ala	Leu	
				80					85					90	
Glu	Asn	Leu	Cys	Glu	Arg	Ile	Leu	Asp	Tyr	Ser	Val	His	Ala	Glu	
				95					100					105	
Arg	Lys	Gly	Ser	Leu	Arg	Tyr	Ala	Lys	Gly	Gln	Ser	Gln	Thr	Met	
				110					115					120	
Ala	Thr	Leu	Lys	Gly	Leu	Val	Gln	Lys	Gly	Val	Lys	Val	Asp	Leu	
				125					130					135	
Gly	Ile	Pro	Leu	Glu	Leu	Leu	Gly								
				140											

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UTRSTUT05
- (B) CLONE: 2879068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64 :

Met	Glu	Asp	Met	Asn	Glu	Tyr	Ser	Asn	Ile	Glu	Glu	Phe	Ala	Glu	
				5					10					15	
Gly	Ser	Lys	Ile	Asn	Ala	Ser	Lys	Asn	Gln	Gln	Asp	Asp	Gly	Lys	
				20					25					30	
Met	Phe	Ile	Gly	Gly	Leu	Ser	Trp	Asp	Thr	Ser	Lys	Lys	Asp	Leu	
				35					40					45	
Thr	Glu	Tyr	Leu	Ser	Arg	Phe	Gly	Glu	Val	Val	Asp	Cys	Thr	Ile	
				50					55					60	
Lys	Thr	Asp	Pro	Val	Thr	Gly	Arg	Ser	Arg	Gly	Phe	Gly	Phe	Val	
				65					70					75	
Leu	Phe	Lys	Asp	Ala	Ala	Ser	Val	Asp	Lys	Val	Leu	Glu	Leu	Lys	
				80					85					90	
Glu	His	Lys	Leu	Asp	Gly	Lys	Leu	Ile	Asp	Pro	Lys	Arg	Ala	Lys	
				95					100					105	
Ala	Leu	Lys	Gly	Lys	Glu	Pro	Pro	Lys	Lys	Val	Phe	Val	Gly	Gly	
				110					115					120	
Leu	Ser	Pro	Asp	Thr	Ser	Glu	Glu	Gln	Ile	Lys	Glu	Tyr	Phe	Gly	

Ala Phe Gly Glu	125	Glu Asn Ile Glu	130	Leu Pro Met Asp Thr	135
Thr Asn Glu Arg	140	Arg Gly Phe Cys Phe	145	Ile Thr Tyr Thr Asp	150
Glu Pro Val Lys	155	Lys Leu Leu Glu Ser	160	Arg Tyr His Gln Ile	165
Ser Gly Lys Cys	170	Glu Ile Lys Val Ala	175	Gln Pro Lys Glu Val	180
Arg Gln Gln Gln	185	Gln Gln Lys Gly	190	Arg Gly Ala Ala	195
Gly Gly Arg Gly	200	Gly Thr Arg Gly Arg	205	Gly Arg Gly Gln Gly	210
Asn Trp Asn Gln	215	Gly Phe Asn Asn Tyr	220	Tyr Asp Gln Gly Tyr	225
Asn Tyr Asn Ser	230	Ala Tyr Gly Gly Asp	235	Gln Asn Tyr Ser Gly	240
Gly Gly Tyr Asp	245	Tyr Thr Gly Tyr Asn	250	Tyr Gly Asn Tyr Gly	255
Gly Gln Gly Tyr	260	Ala Asp Tyr Ser Gly	265	Gln Gln Ser Thr Tyr	270
Lys Ala Ser Arg	275	Gly Gly Asn His	280	Gln Asn Asn Tyr Gln	285
Tyr	290		295		300

## (2) INFORMATION FOR SEQ ID NO: 65:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SINJNOT02
- (B) CLONE: 2886757

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65 :

Met Gly Glu Pro Gln Gln Val Ser Ala	5	Leu Pro Pro Pro Pro Met	15
Gln Tyr Ile Lys Glu Tyr Thr Asp Glu	10	Asn Ile Gln Glu Gly Leu	20
Ala Pro Lys Pro Pro Pro Pro Ile Lys	25	Asp Ser Tyr Met Met Phe	30
Gly Asn Gln Phe Gln Cys Asp Asp Leu	35	Ile Ile Arg Pro Leu Glu	40
Ser Gln Gly Ile Glu Arg Leu His Pro	45	Met Gln Phe Asp His Lys	50
Lys Glu Leu Arg Lys Leu Asn Met Ser	55	Ile Leu Ile Asn Phe Leu	60
Asp Leu Leu Asp Ile Leu Ile Arg Ser	65	Pro Gly Ser Ile Lys Arg	70
Glu Glu Lys Leu Glu Asp Leu Lys Leu	75	Phe Val His Val His	80
His Leu Ile Asn Glu Tyr Arg Pro His	85	Gln Ala Arg Glu Thr Leu	90
Arg Val Met Met Glu Val Gln Lys Arg	95	Gln Arg Leu Glu Thr Ala	100
	110		105
	115		110
	120		115
	125		120
	130		125
	135		130
	140		135
	145		140
			145

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Glu	Arg	Phe	Gln	Lys	His	Leu	Glu	Arg	Val	Ile	Glu	Met	Ile	Gln
				155					160					165
Asn	Cys	Leu	Ala	Ser	Leu	Pro	Asp	Asp	Leu	Pro	His	Ser	Glu	Ala
				170					175					180
Gly	Met	Arg	Val	Lys	Thr	Glu	Pro	Met	Asp	Ala	Asp	Asp	Ser	Asn
				185					190					195
Asn	Cys	Thr	Gly	Gln	Asn	Glu	His	Gln	Arg	Glu	Asn	Ser	Gly	His
				200					205					210
Arg	Arg	Asp	Gln	Ile	Ile	Glu	Lys	Asp	Ala	Ala	Leu	Cys	Val	Leu
				215					220					225
Ile	Asp	Glu	Met	Asn	Glu	Arg	Pro							
				230										

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SCORNOT04
- (B) CLONE: 2964329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66 :

Met	Ala	Gly	Ala	Gly	Ala	Gly	Ala	Gly	Ala	Arg	Gly	Gly	Ala	Ala
				5					10					15
Ala	Gly	Val	Glu	Ala	Arg	Ala	Arg	Asp	Pro	Pro	Pro	Ala	His	Arg
				20					25					30
Ala	His	Pro	Arg	His	Pro	Arg	Pro	Ala	Ala	Gln	Pro	Ser	Ala	Arg
				35					40					45
Arg	Met	Asp	Gly	Gly	Ser	Gly	Gly	Leu	Gly	Ser	Gly	Asp	Asn	Ala
				50					55					60
Pro	Thr	Thr	Glu	Ala	Leu	Phe	Val	Ala	Leu	Gly	Ala	Gly	Val	Thr
				65					70					75
Ala	Leu	Ser	His	Pro	Leu	Leu	Tyr	Val	Lys	Leu	Leu	Ile	Gln	Val
				80					85					90
Gly	His	Glu	Pro	Met	Pro	Pro	Thr	Leu	Gly	Thr	Asn	Val	Leu	Gly
				95					100					105
Arg	Lys	Val	Leu	Tyr	Leu	Pro	Ser	Phe	Phe	Thr	Tyr	Ala	Lys	Tyr
				110					115					120
Ile	Val	Gln	Val	Asp	Gly	Lys	Ile	Gly	Leu	Phe	Arg	Gly	Leu	Ser
				125					130					135
Pro	Arg	Leu	Met	Ser	Asn	Ala	Leu	Ser	Thr	Val	Thr	Arg	Gly	Ser
				140					145					150
Met	Lys	Lys	Val	Phe	Pro	Pro	Asp	Glu	Ile	Glu	Gln	Val	Ser	Asn
				155					160					165
Lys	Asp	Asp	Met	Lys	Thr	Ser	Leu	Lys	Lys	Val	Val	Lys	Glu	Thr
				170					175					180
Ser	Tyr	Glu	Met	Met	Met	Gln	Cys	Val	Ser	Arg	Met	Leu	Ala	His
				185					190					195
Pro	Leu	His	Val	Ile	Ser	Met	Arg	Cys	Met	Val	Gln	Phe	Val	Gly
				200					205					210
Arg	Glu	Ala	Lys	Tyr	Ser	Gly	Val	Leu	Ser	Ser	Ile	Gly	Lys	Ile
				215					220					225
Phe	Lys	Glu	Glu	Gly	Leu	Leu	Gly	Phe	Phe	Val	Gly	Leu	Ile	Pro

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His	Leu	Leu	Gly	230	Asp	Val	Val	Phe	Leu	235	Trp	Gly	Cys	Asn	Leu	240	Leu
Ala	His	Phe	Ile	245	Asn	Ala	Tyr	Leu	Val	250	Asp	Asp	Ser	Phe	Ser	Gln	
Ala	Leu	Ala	Ile	260	Arg	Ser	Tyr	Thr	Lys	265	Phe	Val	Met	Gly	Ile	Ala	
Val	Ser	Met	Leu	275	Thr	Tyr	Pro	Phe	Leu	280	Leu	Val	Gly	Asp	Leu	Met	
Ala	Val	Asn	Asn	290	Cys	Gly	Leu	Gln	Ala	295	Gly	Leu	Pro	Pro	Tyr	Ser	
Pro	Val	Phe	Lys	305	Ser	Trp	Ile	His	Cys	310	Trp	Lys	Tyr	Leu	Ser	Val	
Gln	Gly	Gln	Leu	320	Phe	Arg	Gly	Ser	Ser	325	Leu	Leu	Phe	Arg	Arg	Val	
Ser	Ser	Gly	Ser	335	Cys	Phe	Ala	Leu	Glu	340							
				350													

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SCORNOT04
- (B) CLONE: 2965248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67 :

Met	Ala	Ser	Thr	Ile	Ser	Ala	Tyr	Lys	Glu	Lys	Met	Lys	Glu	Leu			
				5					10					15			
Ser	Val	Leu	Ser	Leu	Ile	Cys	Ser	Cys	Phe	Tyr	Thr	Gln	Pro	His			
				20					25					30			
Pro	Asn	Thr	Val	Tyr	Gln	Tyr	Gly	Asp	Met	Glu	Val	Lys	Gln	Leu			
				35					40					45			
Asp	Lys	Arg	Ala	Ser	Gly	Gln	Ser	Phe	Glu	Val	Ile	Leu	Lys	Ser			
				50					55					60			
Pro	Ser	Asp	Leu	Ser	Pro	Glu	Ser	Pro	Met	Leu	Ser	Ser	Pro	Pro			
				65					70					75			
Lys	Lys	Lys	Asp	Thr	Ser	Leu	Glu	Glu	Leu	Gln	Lys	Arg	Leu	Glu			
				80					85					90			
Ala	Ala	Glu	Glu	Arg	Arg	Lys	Thr	Gln	Glu	Ala	Gln	Val	Leu	Lys			
				95					100					105			
Gln	Leu	Ala	Asp	Gly	Ala	Ser	Thr	Ser	Ala	Arg	Cys	Cys	Thr	Arg			
				110					115					120			
Arg	Trp	Arg	Arg	Ile	Thr	Thr	Ser	Ala	Ala	Arg	Arg	Arg	Arg	Ser			
				125					130					135			
Ser	Thr	Thr	Arg	Trp	Ser	Ser	Ala	Arg	Arg	Ser	Ala	Arg	His	Thr			
				140					145					150			
Trp	Pro	His	Cys	Ala	Ser	Gly	Cys	Ala	Arg	Arg	Ser	Cys	Thr	Arg			
				155					160					165			
Pro	Arg	Cys	Ala	Gly	Thr	Arg	Ser	Ser	Glu	Lys	Arg	Cys	Arg	Ala			
				170					175					180			
Lys	Gly	Pro	Gly	Arg	Ala	Ala	Pro	Ile	Leu	Arg	Arg	Asn	Thr	Phe			
				185					190					195			

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Gly	Phe	Trp	Phe	Cys	Phe	Val	His	Leu	Cys	Leu	Asp	Ala	Thr	Phe
				200					205					210
Val	Pro	Pro	Pro	Pro	Pro	Gln	Pro	Pro	Ala	Ser	Cys	Phe	Ser	Ser
				215					220					225
Ala	Leu	Ser	Arg	Pro	Ala	Leu	Ser	Ser	Trp					
				230					235					

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TLYMNOT06
- (B) CLONE: 3000534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68 :

Met	Trp	Ser	Ala	Gly	Arg	Gly	Gly	Ala	Ala	Trp	Pro	Val	Leu	Leu
				5					10					15
Gly	Leu	Leu	Leu	Ala	Leu	Leu	Val	Pro	Gly	Gly	Gly	Ala	Ala	Lys
				20					25					30
Thr	Gly	Ala	Glu	Leu	Val	Thr	Cys	Gly	Ser	Val	Leu	Lys	Leu	Leu
				35					40					45
Asn	Thr	His	His	Arg	Val	Arg	Leu	His	Ser	His	Asp	Ile	Lys	Tyr
				50					55					60
Gly	Ser	Gly	Ser	Gly	Gln	Gln	Ser	Val	Thr	Gly	Val	Glu	Ala	Ser
				65					70					75
Asp	Asp	Ala	Asn	Ser	Tyr	Trp	Arg	Ile	Arg	Gly	Gly	Ser	Glu	Gly
				80					85					90
Gly	Cys	Pro	Arg	Gly	Ser	Pro	Val	Arg	Cys	Gly	Gln	Ala	Val	Arg
				95					100					105
Leu	Thr	His	Val	Leu	Thr	Gly	Lys	Asn	Leu	His	Thr	His	His	Phe
				110					115					120
Pro	Ser	Pro	Leu	Ser	Asn	Asn	Gln	Glu	Val	Ser	Ala	Phe	Gly	Glu
				125					130					135
Asp	Gly	Glu	Gly	Asp	Asp	Leu	Asp	Leu	Trp	Thr	Val	Arg	Cys	Ser
				140					145					150
Gly	Gln	His	Trp	Glu	Arg	Glu	Ala	Ala	Val	Arg	Phe	Gln	His	Val
				155					160					165
Gly	Thr	Ser	Val	Phe	Leu	Ser	Val	Thr	Gly	Glu	Gln	Tyr	Gly	Ser
				170					175					180
Pro	Ile	Arg	Gly	Gln	His	Glu	Val	His	Gly	Met	Pro	Ser	Ala	Asn
				185					190					195
Thr	His	Asn	Thr	Trp	Lys	Ala	Met	Glu	Gly	Ile	Phe	Ile	Lys	Pro
				200					205					210
Ser	Val	Glu	Pro	Ser	Ala	Gly	His	Asp	Glu	Leu				
				215					220					

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

PF-0459 US

(A) LENGTH: 483 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: HEAANOT01  
(B) CLONE: 3046870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69 :

Met	Lys	Ala	Phe	His	Thr	Phe	Cys	Val	Val	Leu	Leu	Val	Phe	Gly	
				5					10					15	
Ser	Val	Ser	Glu	Ala	Lys	Phe	Asp	Asp	Phe	Glu	Asp	Glu	Glu	Asp	
				20					25					30	
Ile	Val	Glu	Tyr	Asp	Asn	Asp	Phe	Ala	Glu	Phe	Glu	Asp	Val		
				35				40						45	
Met	Glu	Asp	Ser	Val	Thr	Glu	Ser	Pro	Gln	Arg	Val	Ile	Ile	Thr	
				50					55					60	
Glu	Asp	Asp	Glu	Asp	Glu	Thr	Thr	Val	Glu	Leu	Glu	Gly	Gln	Asp	
				65					70					75	
Glu	Asn	Gln	Glu	Gly	Asp	Phe	Glu	Asp	Ala	Asp	Thr	Gln	Glu	Gly	
				80					85					90	
Asp	Thr	Glu	Ser	Glu	Pro	Tyr	Asp	Asp	Glu	Glu	Phe	Glu	Gly	Tyr	
				95					100					105	
Glu	Asp	Lys	Pro	Asp	Thr	Ser	Ser	Ser	Lys	Asn	Lys	Asp	Pro	Ile	
				110					115					120	
Thr	Ile	Val	Asp	Val	Pro	Ala	His	Leu	Gln	Asn	Ser	Trp	Glu	Ser	
				125					130					135	
Tyr	Tyr	Leu	Glu	Ile	Leu	Met	Val	Thr	Gly	Leu	Leu	Ala	Tyr	Ile	
				140					145					150	
Met	Asn	Tyr	Ile	Ile	Gly	Lys	Asn	Lys	Asn	Ser	Arg	Leu	Ala	Gln	
				155					160					165	
Ala	Trp	Phe	Asn	Thr	His	Arg	Glu	Leu	Leu	Glu	Ser	Asn	Phe	Thr	
				170					175					180	
Leu	Val	Gly	Asp	Asp	Gly	Thr	Asn	Lys	Glu	Ala	Thr	Ser	Thr	Gly	
				185					190					195	
Lys	Leu	Asn	Gln	Glu	Asn	Glu	His	Ile	Tyr	Asn	Leu	Trp	Cys	Ser	
				200					205					210	
Gly	Arg	Val	Cys	Cys	Glu	Gly	Met	Leu	Ile	Gln	Leu	Arg	Phe	Leu	
				215					220					225	
Lys	Arg	Gln	Asp	Leu	Leu	Asn	Val	Leu	Ala	Arg	Met	Met	Arg	Pro	
				230					235					240	
Val	Ser	Asp	Gln	Val	Gln	Ile	Lys	Val	Thr	Met	Asn	Asp	Glu	Asp	
				245					250					255	
Met	Asp	Thr	Tyr	Val	Phe	Ala	Val	Gly	Thr	Arg	Lys	Ala	Leu	Val	
				260					265					270	
Arg	Leu	Gln	Lys	Glu	Met	Gln	Asp	Leu	Ser	Glu	Phe	Cys	Ser	Asp	
				275					280					285	
Lys	Pro	Lys	Ser	Gly	Ala	Lys	Tyr	Gly	Leu	Pro	Asp	Ser	Leu	Ala	
				290					295					300	
Ile	Leu	Ser	Glu	Met	Gly	Glu	Val	Thr	Asp	Gly	Met	Met	Asp	Thr	
				305					310					315	
Lys	Met	Val	His	Phe	Leu	Thr	His	Tyr	Ala	Asp	Lys	Ile	Glu	Ser	
				320					325					330	
Val	His	Phe	Ser	Asp	Gln	Phe	Ser	Gly	Pro	Lys	Ile	Met	Gln	Glu	
				335					340					345	
Glu	Gly	Gln	Pro	Leu	Lys	Leu	Pro	Asp	Thr	Lys	Arg	Thr	Leu	Leu	
				350					355					360	
Phe	Thr	Phe	Asn	Val	Pro	Gly	Ser	Gly	Asn	Thr	Tyr	Pro	Lys	Asp	
				365					370					375	



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Met	Glu	Ala	Leu	Leu	Pro	Leu	Met	Asn	Met	Val	Ile	Tyr	Ser	Ile
				380					385					390
Asp	Lys	Ala	Lys	Lys	Phe	Arg	Leu	Asn	Arg	Glu	Gly	Lys	Gln	Lys
				395					400					405
Ala	Asp	Lys	Asn	Arg	Ala	Arg	Val	Glu	Glu	Asn	Phe	Leu	Lys	Leu
				410					415					420
Thr	His	Val	Gln	Arg	Gln	Glu	Ala	Ala	Gln	Ser	Arg	Arg	Glu	Glu
				425					430					435
Lys	Lys	Arg	Ala	Glu	Lys	Glu	Arg	Ile	Met	Asn	Glu	Glu	Asp	Pro
				440					445					450
Glu	Lys	Gln	Arg	Arg	Leu	Glu	Glu	Ala	Ala	Leu	Arg	Arg	Glu	Gln
				455					460					465
Lys	Lys	Leu	Glu	Lys	Lys	Gln	Met	Lys	Met	Lys	Gln	Ile	Lys	Val
				470					475					480
Lys	Ala	Met												

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PONSAT01
- (B) CLONE: 3057669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70 :

Met	Asp	His	Glu	Asp	Ile	Ser	Glu	Ser	Val	Asp	Ala	Ala	Tyr	Asn
				5					10					15
Leu	Gln	Asp	Ser	Cys	Leu	Thr	Asp	Cys	Asp	Val	Glu	Asp	Gly	Thr
				20					25					30
Met	Asp	Gly	Asn	Asp	Glu	Gly	His	Ser	Phe	Glu	Leu	Cys	Pro	Ser
				35					40					45
Glu	Ala	Ser	Pro	Tyr	Val	Arg	Ser	Arg	Glu	Arg	Thr	Ser	Ser	Ser
				50					55					60
Ile	Val	Phe	Glu	Asp	Ser	Gly	Cys	Asp	Asn	Ala	Ser	Ser	Lys	Glu
				65					70					75
Glu	Pro	Lys	Thr	Asn	Arg	Leu	His	Ile	Gly	Asn	His	Cys	Ala	Asn
				80					85					90
Lys	Leu	Thr	Ala	Phe	Lys	Pro	Thr	Ser	Ser	Lys	Ser	Ser	Ser	Glu
				95					100					105
Ala	Thr	Leu	Ser	Ile	Ser	Pro	Pro	Arg	Pro	Thr	Thr	Leu	Ser	Leu
				110					115					120
Asp	Leu	Thr	Lys	Asn	Thr	Thr	Glu	Lys	Leu	Gln	Pro	Ser	Ser	Pro
				125					130					135
Lys	Val	Tyr	Leu	Tyr	Ile	Gln	Met	Gln	Leu	Cys	Arg	Lys	Glu	Asn
				140					145					150
Leu	Lys	Asp	Trp	Met	Asn	Gly	Arg	Cys	Thr	Ile	Glu	Glu	Arg	Glu
				155					160					165
Arg	Ser	Val	Cys	Leu	His	Ile	Phe	Leu	Gln	Ile	Ala	Glu	Ala	Val
				170					175					180
Glu	Phe	Leu	His	Ser	Lys	Gly	Leu	Met	His	Arg	Asp	Leu	Lys	Pro
				185					190					195
Ser	Asn	Ile	Phe	Phe	Thr	Met	Asp	Asp	Val	Val	Lys	Val	Gly	Asp
				200					205					210
Phe	Gly	Leu	Val	Thr	Ala	Met	Asp	Gln	Asp	Glu	Glu	Glu	Gln	Thr

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Val	Leu	Thr	Pro	Met	Pro	Ala	Tyr	Ala	Arg	His	Thr	Gly	Gln	Val
				215					220					225
Gly	Thr	Lys	Leu	Tyr	Met	Ser	Pro	Glu	Gln	Ile	His	Gly	Asn	Ser
				230					235					240
Tyr	Ser	His	Lys	Val	Asp	Ile	Phe	Ser	Leu	Gly	Leu	Ile	Leu	Phe
				245					250					255
Glu	Leu	Leu	Tyr	Pro	Phe	Ser	Thr	Gln	Met	Glu	Arg	Val	Arg	Thr
				260					265					270
Leu	Thr	Asp	Val	Arg	Asn	Leu	Lys	Phe	Pro	Pro	Leu	Phe	Thr	Gln
				275					280					285
Lys	Tyr	Pro	Cys	Glu	Tyr	Val	Met	Val	Gln	Asp	Met	Leu	Ser	Pro
				290					295					300
Ser	Pro	Met	Glu	Arg	Pro	Glu	Ala	Ile	Asn	Ile	Ile	Glu	Asn	Ala
				305					310					315
Val	Phe	Glu	Asp	Leu	Asp	Phe	Pro	Gly	Lys	Thr	Val	Leu	Arg	Gln
				320					325					330
Arg	Ser	Arg	Ser	Leu	Ser	Ser	Ser	Gly	Thr	Lys	His	Ser	Arg	Gln
				335					340					345
Ser	Asn	Asn	Ser	His	Ser	Pro	Leu	Pro	Ser	Asn				360
				350					355					360
				365					370					

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: HEAONOT03
- (B) CLONE: 3088178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71 :

Met	Met	Asn	Asn	Arg	Phe	Arg	Lys	Asp	Met	Met	Lys	Asn	Ala	Ser
				5					10					15
Glu	Ser	Lys	Leu	Ser	Lys	Asp	Asn	Leu	Lys	Lys	Arg	Leu	Lys	Glu
				20					25					30
Glu	Phe	Gln	His	Ala	Met	Gly	Gly	Val	Pro	Ala	Trp	Ala	Glu	Thr
				35					40					45
Thr	Lys	Arg	Lys	Thr	Ser	Ser	Asp	Asp	Glu	Ser	Glu	Glu	Asp	Glu
				50					55					60
Asp	Asp	Leu	Leu	Gln	Arg	Thr	Gly	Asn	Phe	Ile	Ser	Thr	Ser	Thr
				65					70					75
Ser	Leu	Pro	Arg	Gly	Ile	Leu	Lys	Met	Lys	Asn	Cys	Gln	His	Ala
				80					85					90
Asn	Ala	Glu	Arg	Pro	Thr	Val	Ala	Arg	Ile	Ser	Ser	Val	Gln	Phe
				95					100					105
His	Pro	Gly	Ala	Gln	Ile	Val	Met	Val	Ala	Gly	Leu	Asp	Asn	Ala
				110					115					120
Val	Ser	Leu	Phe	Gln	Val	Asp	Gly	Lys	Thr	Asn	Pro	Lys	Ile	Gln
				125					130					135
Ser	Ile	Tyr	Leu	Glu	Arg	Phe	Pro	Ile	Phe	Lys	Ala	Cys	Phe	Ser
				140					145					150
Ala	Asn	Gly	Glu	Glu	Val	Leu	Ala	Thr	Ser	Thr	His	Ser	Lys	Val
				155					160					165

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Leu	Tyr	Val	Tyr	Asp	Met	Leu	Ala	Gly	Lys	Leu	Ile	Pro	Val	His
				170					175					180
Gln	Val	Arg	Gly	Leu	Lys	Glu	Lys	Ile	Val	Arg	Ser	Phe	Glu	Val
				185					190					195
Ser	Pro	Asp	Gly	Ser	Phe	Leu	Leu	Ile	Asn	Gly	Ile	Ala	Gly	Tyr
				200					205					210
Leu	His	Leu	Leu	Ala	Met	Lys	Thr	Lys	Glu	Leu	Ile	Gly	Ser	Met
				215					220					225
Lys	Ile	Asn	Gly	Arg	Val	Ala	Ala	Ser	Thr	Phe	Ser	Ser	Asp	Ser
				230					235					240
Lys	Lys	Val	Tyr	Ala	Ser	Ser	Gly	Asp	Gly	Glu	Val	Tyr	Val	Trp
				245					250					255
Asp	Val	Asn	Ser	Arg	Lys	Cys	Leu	Asn	Arg	Phe	Val	Asp	Glu	Gly
				260					265					270
Ser	Leu	Tyr	Gly	Leu	Ser	Ile	Ala	Thr	Ser	Arg	Asn	Gly	Gln	Tyr
				275					280					285
Val	Ala	Cys	Gly	Ser	Asn	Cys	Gly	Val	Val	Asn	Ile	Tyr	Asn	Gln
				290					295					300
Asp	Ser	Cys	Leu	Gln	Glu	Thr	Asn	Pro	Lys	Pro	Ile	Lys	Ala	Ile
				305					310					315
Met	Asn	Leu	Val	Thr	Gly	Val	Thr	Ser	Leu	Thr	Phe	Asn	Pro	Thr
				320					325					330
Thr	Glu	Ile	Leu	Ala	Ile	Ala	Ser	Glu	Lys	Met	Lys	Glu	Ala	Val
				335					340					345
Arg	Leu	Val	His	Leu	Pro	Ser	Cys	Thr	Val	Phe	Ser	Asn	Phe	Pro
				350					355					360
Val	Ile	Lys	Asn	Lys	Asn	Ile	Ser	His	Val	His	Thr	Met	Asp	Phe
				365					370					375
Ser	Pro	Arg	Ser	Gly	Tyr	Phe	Ala	Leu	Gly	Asn	Glu	Lys	Gly	Lys
				380					385					390
Ala	Leu	Met	Tyr	Arg	Leu	His	His	Tyr	Ser	Asp	Phe			
				395					400					

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT19
- (B) CLONE: 3094321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72 :

Met	Ala	Leu	Ser	Arg	Gly	Leu	Pro	Arg	Glu	Leu	Ala	Glu	Ala	Val
				5					10					15
Ala	Gly	Gly	Arg	Val	Leu	Val	Val	Gly	Ala	Gly	Gly	Ile	Gly	Cys
				20					25					30
Glu	Leu	Leu	Lys	Asn	Leu	Val	Leu	Thr	Gly	Phe	Ser	His	Ile	Asp
				35					40					45
Leu	Ile	Asp	Leu	Asp	Thr	Ile	Asp	Val	Ser	Asn	Leu	Asn	Arg	Gln
				50					55					60
Phe	Leu	Phe	Gln	Lys	Lys	His	Val	Gly	Arg	Ser	Lys	Ala	Gln	Val
				65					70					75
Ala	Lys	Glu	Ser	Val	Leu	Gln	Phe	Tyr	Pro	Lys	Ala	Asn	Ile	Val

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				80					85				90	
Ala	Tyr	His	Asp	Ser	Ile	Met	Asn	Pro	Asp	Tyr	Asn	Val	Glu	Phe
				95					100					105
Phe	Arg	Gln	Phe	Ile	Leu	Val	Met	Asn	Ala	Leu	Asp	Asn	Arg	Ala
				110					115					120
Ala	Arg	Asn	His	Val	Asn	Arg	Met	Cys	Leu	Ala	Ala	Asp	Val	Pro
				125					130					135
Leu	Ile	Glu	Ser	Gly	Thr	Ala	Gly	Tyr	Leu	Gly	Gln	Val	Thr	Thr
				140					145					150
Ile	Lys	Lys	Gly	Val	Thr	Glu	Cys	Tyr	Glu	Cys	His	Pro	Lys	Pro
				155					160					165
Thr	Gln	Arg	Thr	Phe	Pro	Gly	Cys	Thr	Ile	Arg	Asn	Thr	Pro	Ser
				170					175					180
Glu	Pro	Ile	His	Cys	Ile	Val	Trp	Ala	Lys	Tyr	Leu	Phe	Asn	Gln
				185					190					195
Leu	Phe	Gly	Glu	Glu	Asp	Ala	Asp	Gln	Glu	Val	Ser	Pro	Asp	Arg
				200					205					210
Ala	Asp	Pro	Glu	Ala	Ala	Trp	Glu	Pro	Thr	Glu	Ala	Glu	Ala	Arg
				215					220					225
Ala	Arg	Ala	Ser	Asn	Glu	Asp	Gly	Asp	Ile	Lys	Arg	Ile	Ser	Thr
				230					235					240
Lys	Glu	Trp	Ala	Lys	Ser	Thr	Gly	Tyr	Asp	Pro	Val	Lys	Leu	Phe
				245					250					255
Thr	Lys	Leu	Phe	Lys	Asp	Asp	Ile	Arg	Tyr	Leu	Leu	Thr	Met	Asp
				260					265					270
Lys	Leu	Trp	Arg	Lys	Arg	Lys	Pro	Pro	Val	Pro	Leu	Asp	Trp	Ala
				275					280					285
Glu	Val	Gln	Ser	Gln	Gly	Glu	Glu	Thr	Asn	Ala	Ser	Asp	Gln	Gln
				290					295					300
Asn	Glu	Pro	Gln	Leu	Gly	Leu	Lys	Asp	Gln	Gln	Val	Leu	Asp	Val
				305					310					315
Lys	Ser	Tyr	Ala	Arg	Leu	Phe	Ser	Lys	Ser	Ile	Glu	Thr	Leu	Arg
				320					325					330
Val	His	Leu	Ala	Glu	Lys	Gly	Asp	Gly	Ala	Glu	Leu	Ile	Trp	Asp
				335					340					345
Lys	Asp	Asp	Pro	Ser	Ala	Met	Asp	Phe	Val	Thr	Ser	Ala	Ala	Asn
				350					355					360
Leu	Arg	Met	His	Ile	Phe	Ser	Met	Asn	Met	Lys	Ser	Arg	Phe	Asp
				365					370					375
Ile	Lys	Ser	Met	Ala	Gly	Asn	Ile	Ile	Pro	Ala	Ile	Ala	Thr	Thr
				380					385					390
Asn	Ala	Val	Ile	Ala	Gly	Leu	Ile	Val	Leu	Glu	Gly	Leu	Lys	Ile
				395					400					405
Leu	Ser	Gly	Lys	Ile	Asp	Gln	Cys	Arg	Thr	Ile	Phe	Leu	Asn	Lys
				410					415					420
Gln	Pro	Asn	Pro	Arg	Lys	Lys	Leu	Leu	Val	Pro	Cys	Ala	Leu	Asp
				425					430					435
Pro	Pro	Asn	Pro	Asn	Cys	Tyr	Val	Cys	Ala	Ser	Lys	Pro	Glu	Val
				440					445					450
Thr	Val	Arg	Leu	Asn	Val	His	Lys	Val	Thr	Val	Leu	Thr	Leu	Gln
				455					460					465
Asp	Lys	Ile	Val	Lys	Glu	Lys	Phe	Ala	Met	Val	Ala	Pro	Asp	Val
				470					475					480
Gln	Ile	Glu	Asp	Gly	Lys	Gly	Thr	Ile	Leu	Ile	Ser	Ser	Glu	Glu
				485					490					495
Gly	Glu	Thr	Glu	Ala	Asn	Asn	His	Lys	Lys	Leu	Ser	Glu	Phe	Gly
				500					505					510
Ile	Arg	Asn	Gly	Ser	Arg	Leu	Gln	Ala	Asp	Asp	Phe	Leu	Gln	Asp
				515					520					525
Tyr	Thr	Leu	Leu	Ile	Asn	Ile	Leu	His	Ser	Glu	Asp	Leu	Gly	Lys
				530					535					540

[illegible]

(2) INFORMATION FOR SEQ ID NO: 73:

(A) LENGTH: 237 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(A) LIBRARY: LUNGTUT13  
(B) CLONE: 3115936

## 186

	215		220	225
Arg Gly Lys Glu	Asp	Ala Gly Lys Ala	Phe	Ala Ser
	230		235	

## (2) INFORMATION FOR SEQ ID NO: 74:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT13  
 (B) CLONE: 3116522

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74 :

Met	Asp	Ala	Arg	Trp	Trp	Ala	Val	Val	Val	Leu	Ala	Ala	Phe	Pro	5	10	15
Ser	Leu	Gly	Ala	Gly	Gly	Glu	Thr	Pro	Glu	Ala	Pro	Pro	Glu	Ser	20	25	30
Trp	Thr	Gln	Leu	Trp	Phe	Phe	Arg	Phe	Val	Val	Asn	Ala	Ala	Gly	35	40	45
Tyr	Ala	Ser	Phe	Met	Val	Pro	Gly	Tyr	Leu	Leu	Val	Gln	Tyr	Phe	50	55	60
Arg	Arg	Lys	Asn	Tyr	Leu	Glu	Thr	Gly	Arg	Gly	Leu	Cys	Phe	Pro	65	70	75
Leu	Val	Lys	Ala	Cys	Val	Phe	Gly	Asn	Glu	Pro	Lys	Ala	Ser	Asp	80	85	90
Glu	Val	Pro	Leu	Ala	Pro	Arg	Thr	Glu	Ala	Ala	Glu	Thr	Thr	Pro	95	100	105
Met	Trp	Gln	Ala	Leu	Lys	Leu	Leu	Phe	Cys	Ala	Thr	Gly	Leu	Gln	110	115	120
Val	Ser	Tyr	Leu	Thr	Trp	Gly	Val	Leu	Gln	Glu	Arg	Val	Met	Thr	125	130	135
Arg	Ser	Tyr	Gly	Ala	Thr	Ala	Thr	Ser	Pro	Gly	Glu	Arg	Phe	Thr	140	145	150
Asp	Ser	Gln	Phe	Leu	Val	Leu	Met	Asn	Arg	Val	Leu	Ala	Leu	Ile	155	160	165
Val	Ala	Gly	Leu	Ser	Cys	Val	Leu	Cys	Lys	Gln	Pro	Arg	His	Gly	170	175	180
Ala	Pro	Met	Tyr	Arg	Tyr	Ser	Phe	Ala	Ser	Leu	Ser	Asn	Val	Leu	185	190	195
Ser	Ser	Trp	Cys	Gln	Tyr	Glu	Ala	Leu	Lys	Phe	Val	Ser	Phe	Pro	200	205	210
Thr	Gln	Val	Leu	Ala	Lys	Ala	Ser	Lys	Val	Ile	Pro	Val	Met	Leu	215	220	225
Met	Gly	Lys	Leu	Val	Ser	Arg	Arg	Ser	Tyr	Glu	His	Trp	Glu	Tyr	230	235	240
Leu	Thr	Ala	Thr	Leu	Ile	Ser	Ile	Gly	Val	Ser	Met	Phe	Leu	Leu	245	250	255
Ser	Ser	Gly	Pro	Glu	Pro	Arg	Ser	Ser	Pro	Ala	Thr	Thr	Leu	Ser	260	265	270
Gly	Leu	Ile	Leu	Leu	Ala	Gly	Tyr	Ile	Ala	Phe	Asp	Ser	Phe	Thr	275	280	285
Ser	Asn	Trp	Gln	Asp	Ala	Leu	Phe	Ala	Tyr	Lys	Met	Ser	Ser	Val	290	295	300

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Gln	Met	Met	Phe	Gly	Val	Asn	Phe	Phe	Ser	Cys	Leu	Phe	Thr	Val	
				305					310					315	
Gly	Ser	Leu	Leu	Glu	Gln	Gly	Ala	Leu	Leu	Glu	Gly	Thr	Arg	Phe	
				320					325					330	
Met	Gly	Arg	His	Ser	Glu	Phe	Ala	Ala	His	Ala	Leu	Leu	Leu	Ser	
				335					340					345	
Ile	Cys	Ser	Ala	Cys	Gly	Gln	Leu	Phe	Ile	Phe	Tyr	Thr	Ile	Gly	
				350					355					360	
Gln	Phe	Gly	Ala	Ala	Val	Phe	Thr	Ile	Ile	Met	Thr	Leu	Arg	Gln	
				365					370					375	
Ala	Phe	Ala	Ile	Leu	Leu	Ser	Cys	Leu	Leu	Tyr	Gly	His	Thr	Val	
				380					385					390	
Thr	Val	Val	Gly	Gly	Leu	Gly	Val	Ala	Val	Val	Phe	Ala	Ala	Leu	
				395					400					405	
Leu	Leu	Arg	Val	Tyr	Ala	Arg	Gly	Arg	Leu	Lys	Gln	Arg	Gly	Lys	
				410					415					420	
Lys	Ala	Val	Pro	Val	Glu	Ser	Pro	Val	Gln	Lys	Val				
				425					430						

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT13
- (B) CLONE: 3117184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75 :

Met	Ser	Phe	Pro	Pro	His	Leu	Asn	Arg	Pro	Pro	Met	Gly	Ile	Pro	
				5					10					15	
Ala	Leu	Pro	Pro	Gly	Thr	Pro	Pro	Pro	Gln	Phe	Pro	Gly	Phe	Pro	
				20					25					30	
Pro	Pro	Val	Pro	Pro	Gly	Thr	Pro	Met	Ile	Pro	Val	Pro	Met	Ser	
				35					40					45	
Ile	Met	Ala	Pro	Ala	Pro	Thr	Val	Leu	Val	Pro	Thr	Val	Ser	Met	
				50					55					60	
Val	Gly	Lys	His	Leu	Gly	Ala	Arg	Lys	Asp	His	Pro	Gly	Leu	Lys	
				65					70					75	
Ala	Lys	Glu	Asn	Asp	Glu	Asn	Cys	Gly	Pro	Thr	Thr	Thr	Val	Phe	
				80					85					90	
Val	Gly	Asn	Ile	Ser	Glu	Lys	Ala	Ser	Asp	Met	Leu	Ile	Arg	Gln	
				95					100					105	
Leu	Leu	Ala	Lys	Cys	Gly	Leu	Val	Leu	Ser	Trp	Lys	Arg	Val	Gln	
				110					115					120	
Gly	Ala	Ser	Gly	Lys	Leu	Gln	Ala	Phe	Gly	Phe	Cys	Glu	Tyr	Lys	
				125					130					135	
Glu	Pro	Glu	Ser	Thr	Leu	Arg	Ala	Leu	Arg	Leu	Leu	His	Asp	Leu	
				140					145					150	
Gln	Ile	Gly	Glu	Lys	Lys	Leu	Leu	Val	Lys	Val	Asp	Ala	Lys	Thr	
				155					160					165	
Lys	Ala	Gln	Leu	Asp	Glu	Trp	Lys	Ala	Lys	Lys	Lys	Ala	Ser	Asn	
				170					175					180	
Gly	Asn	Ala	Arg	Pro	Glu	Thr	Val	Thr	Asn	Asp	Asp	Glu	Glu	Ala	

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Leu Asp Glu Glu Thr	185	Lys Arg Arg Asp	190	Gln Met Ile Lys Gly	195
	200		205		210
Ile Glu Val Leu Ile	215	Arg Glu Tyr Ser	220	Ser Glu Leu Asn Ala	225
Ser Gln Glu Ser Asp	230	Ser His Pro Arg	235	Lys Lys Lys Lys Glu	240
Lys Glu Asp Ile Phe	245	Gly Arg Phe Gln	250	Trp Ala His	

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LNODNOT05
- (B) CLONE: 3125156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76 :

Met Gly Pro Gln Ala	5	Ala Pro Leu Thr	10	Ile Arg Gly Pro Ser	15
Ala Gly Gln Ser Thr	20	Pro Ser Pro His	25	Leu Val Pro Ser Pro	30
Pro Ser Pro Gly Pro	35	Gly Pro Val Pro	40	Pro Arg Pro Pro Ala	45
Glu Pro Pro Pro Cys	50	Leu Arg Arg Gly	55	Ala Ala Ala Asp Leu	60
Leu Ser Ser Ser Pro	65	Glu Ser Gln His	70	Gly Gly Thr Gln Ser	75
Gly Gly Gly Gln Pro	80	Leu Leu Gln Pro	85	Thr Lys Val Asp Ala	90
Glu Gly Arg Arg Pro	95	Gln Ala Leu Arg	100	Leu Ile Glu Arg Asp	105
Tyr Glu His Pro Glu	110	Arg Leu Arg Gln	115	Leu Gln Gln Glu Leu	120
Ala Phe Arg Gly Gln	125	Leu Gly Asp Val	130	Gly Ala Leu Asp Thr	135
Trp Arg Glu Leu Gln	140	Asp Ala Gln Glu	145	His Asp Ala Arg Gly	150
Ser Ile Ala Ile Ala	155	Arg Cys Tyr Ser	160	Leu Lys Asn Arg His	165
Asp Val Met Pro Tyr	170	Asp Ser Asn Arg	175	Val Val Leu Arg Ser	180
Lys Asp Asp Tyr Ile	185	Asn Ala Ser Cys	190	Val Glu Gly Leu Ser	195
Tyr Cys Pro Pro Leu	200	Val Ala Thr Gln	205	Ala Pro Leu Pro Gly	210
Ala Ala Asp Phe Trp	215	Leu Met Val His	220	Glu Gln Lys Val Ser	225
Ile Val Met Leu Val	230	Ser Glu Ala Glu	235	Met Glu Lys Gln Lys	240
Ala Arg Tyr Phe Pro	245	Thr Glu Arg Gly	250	Gln Pro Met Val His	255



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Ala	Leu	Ser	Leu	Ala	Leu	Ser	Ser	Val	Arg	Ser	Thr	Glu	Thr	His
				260					265					270
Val	Glu	Arg	Val	Leu	Ser	Leu	Gln	Phe	Arg	Asp	Gln	Ser	Leu	Lys
				275					280					285
Arg	Ser	Leu	Val	His	Leu	His	Phe	Pro	Thr	Trp	Pro	Glu	Leu	Gly
				290					295					300
Leu	Pro	Asp	Ser	Pro	Ser	Asn	Leu	Leu	Arg	Phe	Ile	Gln	Glu	Val
				305					310					315
His	Ala	His	Tyr	Leu	His	Gln	Arg	Pro	Leu	His	Thr	Pro	Ile	Ile
				320					325					330
Val	His	Cys	Ser	Ser	Gly	Val	Gly	Arg	Thr	Gly	Ala	Phe	Ala	Leu
				335					340					345
Leu	Tyr	Ala	Ala	Val	Gln	Glu	Val	Glu	Ala	Gly	Asn	Gly	Ile	Pro
				350					355					360
Glu	Leu	Pro	Gln	Leu	Val	Arg	Arg	Met	Arg	Gln	Gln	Arg	Lys	His
				365					370					375
Met	Leu	Gln	Glu	Lys	Leu	His	Leu	Arg	Phe	Cys	Tyr	Glu	Ala	Val
				380					385					390
Val	Arg	His	Val	Glu	Gln	Val	Leu	Gln	Arg	His	Gly	Val	Pro	Pro
				395					400					405
Pro	Cys	Lys	Pro	Leu	Ala	Ser	Ala	Ser	Ile	Ser	Gln	Lys	Asn	His
				410					415					420
Leu	Pro	Gln	Asp	Ser	Gln	Asp	Leu	Val	Leu	Gly	Gly	Asp	Val	Pro
				425					430					435
Ile	Ser	Ser	Ile	Gln	Ala	Thr	Ile	Ala	Lys	Leu	Ser	Ile	Arg	Pro
				440					445					450
Pro	Gly	Gly	Leu	Glu	Ser	Pro	Val	Ala	Ser	Leu	Pro	Gly	Pro	Ala
				455					460					465
Glu	Pro	Pro	Gly	Leu	Pro	Pro	Ala	Ser	Leu	Pro	Glu	Ser	Thr	Pro
				470					475					480
Ile	Pro	Ser	Ser	Ser	Gln	Thr	Pro	Phe	Pro	Pro	His	Tyr	Leu	Arg
				485					490					495
Leu	Pro	Ser	Leu	Arg	Arg	Ser	Arg	Gln	Cys	Leu	Lys	Pro	Pro	Ala
				500					505					510
Arg	Gly	Pro	Pro	Pro	Pro	Pro	Trp	Asn	Cys	Trp	Pro	Pro		
				515					520					

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT12
- (B) CLONE: 3129120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77 :

Met	Gly	Leu	Leu	Ser	Asp	Pro	Val	Arg	Arg	Arg	Ala	Leu	Ala	Arg
				5					10					15
Leu	Val	Leu	Arg	Leu	Asn	Ala	Pro	Leu	Cys	Val	Leu	Ser	Tyr	Val
				20					25					30
Ala	Gly	Ile	Ala	Trp	Phe	Leu	Ala	Leu	Val	Phe	Pro	Pro	Leu	Thr
				35					40					45
Gln	Arg	Thr	Tyr	Met	Ser	Glu	Asn	Ala	Met	Gly	Ser	Thr	Met	Val
				50					55					60

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Glu	Glu	Gln	Phe	Ala	Gly	Gly	Asp	Arg	Ala	Arg	Ala	Phe	Ala	Arg	
				65					70					75	
Asp	Phe	Ala	Ala	His	Arg	Lys	Lys	Ser	Gly	Ala	Leu	Pro	Val	Ala	
				80					85					90	
Trp	Leu	Glu	Arg	Thr	Met	Arg	Ser	Val	Gly	Leu	Glu	Val	Tyr	Thr	
				95					100					105	
Gln	Ser	Phe	Ser	Arg	Lys	Leu	Pro	Phe	Pro	Asp	Glu	Thr	His	Glu	
				110					115					120	
Arg	Tyr	Met	Val	Ser	Gly	Thr	Asn	Val	Tyr	Gly	Ile	Leu	Arg	Ala	
				125					130					135	
Pro	Arg	Ala	Ala	Ser	Thr	Glu	Ser	Leu	Val	Leu	Thr	Val	Pro	Cys	
				140					145					150	
Gly	Ser	Asp	Ser	Thr	Asn	Ser	Gln	Ala	Val	Gly	Leu	Leu	Leu	Ala	
				155					160					165	
Leu	Ala	Ala	His	Phe	Arg	Gly	Gln	Ile	Tyr	Trp	Ala	Lys	Asp	Ile	
				170					175					180	
Val	Phe	Leu	Val	Thr	Glu	His	Asp	Leu	Leu	Gly	Thr	Glu	Ala	Trp	
				185					190					195	
Leu	Glu	Ala	Tyr	His	Asp	Val	Asn	Val	Thr	Gly	Met	Gln	Ser	Ser	
				200					205					210	
Pro	Leu	Gln	Gly	Arg	Ala	Gly	Ala	Ile	Gln	Ala	Ala	Val	Ala	Leu	
				215					220					225	
Glu	Leu	Ser	Ser	Asp	Val	Val	Thr	Ser	Leu	Asp	Val	Ala	Val	Glu	
				230					235					240	
Gly	Leu	Asn	Gly	Gln	Leu	Pro	Asn	Leu	Asp	Leu	Leu	Asn	Leu	Phe	
				245					250					255	
Gln	Thr	Phe	Cys	Gln	Lys	Gly	Gly	Leu	Leu	Cys	Thr	Leu	Gln	Gly	
				260					265					270	
Lys	Leu	Gln	Pro	Glu	Asp	Trp	Thr	Ser	Leu	Asp	Gly	Pro	Leu	Gln	
				275					280					285	
Gly	Leu	Gln	Thr	Leu	Leu	Leu	Met	Val	Leu	Arg	Gln	Ala	Ser	Gly	
				290					295					300	
Arg	Pro	His	Gly	Ser	His	Gly	Leu	Phe	Leu	Arg	Tyr	Arg	Val	Glu	
				305					310					315	
Ala	Leu	Thr	Leu	Arg	Gly	Ile	Asn	Ser	Phe	Arg	Gln	Tyr	Lys	Tyr	
				320					325					330	
Asp	Leu	Val	Ala	Val	Gly	Lys	Ala	Leu	Glu	Gly	Met	Phe	Arg	Lys	
				335					340					345	
Leu	Asn	His	Leu	Leu	Glu	Arg	Leu	His	Gln	Ser	Phe	Phe	Leu	Tyr	
				350					355					360	
Leu	Leu	Pro	Gly	Leu	Ser	Arg	Phe	Val	Ser	Ile	Gly	Leu	Tyr	Met	
				365					370					375	
Pro	Ala	Val	Gly	Phe	Leu	Leu	Leu	Val	Leu	Gly	Leu	Lys	Ala	Leu	
				380					385					390	
Glu	Leu	Trp	Met	Gln	Leu	His	Glu	Ala	Gly	Met	Gly	Leu	Glu	Glu	
				395					400					405	
Pro	Gly	Gly	Ala	Pro	Gly	Pro	Ser	Val	Pro	Leu	Pro	Pro	Ser	Gln	
				410					415					420	
Gly	Val	Gly	Leu	Ala	Ser	Leu	Val	Ala	Pro	Leu	Leu	Ile	Ser	Gln	
				425					430					435	
Ala	Met	Gly	Leu	Ala	Leu	Tyr	Val	Leu	Pro	Val	Leu	Gly	Gln	His	
				440					445					450	
Val	Ala	Thr	Gln	His	Phe	Pro	Val	Ala	Glu	Ala	Glu	Ala	Val	Val	
				455					460					465	
Leu	Thr	Leu	Leu	Ala	Ile	Tyr	Ala	Ala	Gly	Leu	Ala	Leu	Pro	His	
				470					475					480	
Asn	Thr	His	Arg	Val	Val	Ser	Thr	Gln	Ala	Pro	Asp	Arg	Gly	Trp	
				485					490					495	
Met	Ala	Leu	Lys	Leu	Val	Ala	Leu	Ile	Tyr	Leu	Ala	Leu	Gln	Leu	
				500					505					510	
Gly	Cys	Ile	Ala	Leu	Thr	Asn	Phe	Ser	Leu	Gly	Phe	Leu	Leu	Ala	

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Thr Thr Met Val	515	Pro Thr Ala Ala Leu	520	Ala Lys Pro His Gly	525
Arg Thr Leu Tyr	530	Ala Ala Leu Leu Val	535	Leu Thr Ser Pro Ala	540
Thr Leu Leu Gly	545	Ser Leu Phe Leu Trp	550	Arg Glu Leu Gln Glu	555
Pro Leu Ser Leu	560	Ala Glu Gly Trp Gln	565	Leu Phe Leu Ala Ala	570
Ala Gln Gly Val	575	Leu Glu His His Thr	580	Tyr Gly Ala Leu Leu	585
Pro Leu Leu Ser	590	Leu Gly Leu Tyr Pro	595	Cys Trp Leu Leu Phe	600
Asn Val Leu Phe	605	Trp Lys	610		615
	620				

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: HEARNOT01
- (B) CLONE: 305841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78 :

CCCTCGAGAA GATGGCGGCG ACTCTGGGAC CCCTTGGGTC GTGGCAGCAG TGGCGGCGAT 60  
GTTTGTCTGGC TCGGGATGGG TCCAGGATGT TACTCCTTCT TCTTTTGTG GGGTCTGGGC 120  
AGGGGCCACA GCAAGTCGGG GCGGGTCAAA CGTTCGAGTA CTTGAAACGG GAGCACTCGC 180  
TGTCGAAGCC CTACCAGGGT GTGGGCACAG GCAGTTCCTC ACTGTGGAAT CTGATGGGCA 240  
ATGCCATGGT GATGACCCAG TATATCCGCC TTACCCCAAGA TATGCAAAGT AAACAGGGTG 300  
CCTTGTGGAA CCGGGTGCCA TGTTTCCTGA GAGACTGGGA GTTGCAGGTG CACTTCAAAA 360  
TCCATGGACA AGGAAAGAAG AATCTGCATG GGGATGGCTT GGCAATCTGG TACACAAAGG 420  
ATCGGATGCA GCCAGGGCCT GTGTTTGGAA ACATGGACAA ATTTGTGGGG CTGGGAGTAT 480  
TTGTAGACAC CTACCCCAAT GAGGAGAAGC AGCAAGAGCG GGTATTCCCC TACATCTCAG 540  
CCATGGTGAA CAACGGCTCC CTCAGCTATG ATCATGAGCG GGATGGGCGG CCTACAGAGC 600  
TGGGAGGCTG CACAGCCATT GTCCGCAATC TTCATTACGA CACCTTCCTG GTGATTCGCT 660  
ACGTCAAGAG GCATTTGACG ATAATGATGG ATATTGATGG CAAGCATGAG TGGAGGGACT 720  
GCATTGAAGT GCCCGGAGTC CGCCTGCCCC GCGGCTACTA CTTCCGCACC TCCTCCATCA 780  
CTGGGGATCT CTCAGATAAT CATGATGTCA TTTCTTGAA GTTGTGTTGAA CTGACAGTGG 840

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AGAGAACCCC AGAAGAGGAA AAGCTCCATC GAGATGTGTT CTTGCCCTCA GTGGACAATA 900  
TGAAGCTGCC TGAGATGACA GCTCCACTGC CGCCCCTGAG TGGCCTGGCC CTCTTCCTCA 960  
TCGTCTTTTT CTCCCTGGTG TTTTCTGTAT TTGCCATAGT CATTGGTATC ATACTCTACA 1020  
ACAAATGGCA GGAACAGAGC CGAAAGCGCT TCTACTGAGC CCTCCTGCTG CCACCACTTT 1080  
TGTGACTGTC ACCCATGAGG TATGGAAGGA GCAGGCACTG GCCTGAGCAT GCAGCCTGGA 1140  
GAGTGTTCCT GTCTCTAGCA GCTGGTTGGG GACTATATTC TGTCACCTGA GTTTTGAATG 1200  
CAGGGACCCC GCATTCCCAT GGTGTGTCAT GGGGACATCT AACTCTGGTC TGGGAAGCCA 1260  
CCCACCCCAG GGCAATGCTG CTGTGATGTG CCTTTCCTG CAGTCCTTCC ATGTGGGAGC 1320  
AGAGGTGTGA AGAGAATTTA CGTGGTTGTG ATGCCAAAAT CACAGAACAG AATTTTCATAG 1380  
CCCAGGCTGC CGTGTGTGTTT GACTCAGAAG GCCCTTCTAC TTCAGTTTTG AATCCACAAA 1440  
GAATTAAAAA CTGGTAACAC CACAGGCTTT CTGACCATCC ATTCGTTGGG TTTTGCATTT 1500  
GACCCAACCC TCTGCCTACC TGAGGAGCTT TCTTTGGAAA CCAGGATGGA AACTTCTTCC 1560  
CTGCCTTACC TTCCTTTCAC TCCATTCAAT GTCCTCTCTG TGTGCAACCT GAGCTGGGAA 1620  
AGGCATTGCG ATGCCTCTCT GTTGGGGCCT GGGGCTGCAG AACACACCTG CGTTTCACTG 1680  
GCCTTCATTA GGTGGCCCTA GGGAGATGGC TTTCTGCTTT GGATCACTGT TCCCTAGCAT 1740  
GGGTCTTGGG TCTATTGGCA TGTCCATGGC CTTCCCAATC AAGTCTCTTC AGGCCCTCAG 1800  
TGAAGTTTGG CTAAAGGTTG GTGTAAAAAT CAAGAGAAGC CTGGAAGACA TCATGGATGC 1860  
CATGGATTAG CTGTGCAACT GACCAGCTCC AGGTTTGATC AAACCAAAG CAACATTTGT 1920  
CATGTGGTCT GACCATGTGG AGATGTTTCT GGACTTGCTA GAGCCTGCTT AGCTGCATGT 1980  
TTTGTAGTTA CGATTTTTGG AATCCCACTT TGAGTGCTGA AAGTGTAAGG AAGCTTTCTT 2040  
CTTACACCTT GGGCTTGGAT ATTGCCAGA GAAGAAATTT GGCTTTTTTT TTCTTAATGG 2100  
ACAAGAGACA GTTGCTGTTC TCATGTTCCA AGTCTGAGAG CAACAGACCC TCATCATCTG 2160  
TGCCTGGAAG AGTTCACTGT CATTGAGCAG CACAGCCTGA GTGCTGGCCT CTGTCAACCC 2220  
TTATTCCACT GCCTTATTTG ACAAGGGGTT ACATGCTGCT CACCTTACTG CCCTGGGATT 2280  
AAATCAGTTA CAGGCCAGAG TCTCCTTGGA GGGCCTGGAA CTCTGAGTCC TCCTATGAAC 2340  
CTCTGTA 2347

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1529 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: EOSIHET02  
(B) CLONE: 322866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79 :

CCCACGCGTC CGCCAGCCTT GTCTCGGCCA CCTCAAGGAT AATCACTAAA TTCTGCCGAA 60  
AGGACTGAGG AACGGTGCCT GGAAAAGGGC AAGAATATCA CGGCATGGGC ATGAGTAGCT 120  
TGAAACTGCT GAAGTATGTC CTGTTTTTCT TCAACTTGCT CTTTGGATC TGTGGCTGCT 180  
GCATTTTGGG CTTTGGGATC TACCTGCTGA TCCACAACAA CTTGGAGTG CTCTCCATA 240  
ACCTGCCCTC CCTCACGCTG GGCAATGTGT TTGTCATCGT GGGCTCTATT ATCATGGTAG 300  
TTGCCTTCCT GGGCTGCATG GGCTCTATCA AGGAAAACAA GTGTCTGCTT ATGTCGTTCT 360  
TCATCCTGCT GCTGATTATC CTCCTTGCTG AGGTGACCTT GGCCATCCTG CTCTTTGTAT 420  
ATGAACAGAA GCTGAATGAG TATGTGGCTA AGGGTCTGAC CGACAGCATC CACCGTTACC 480  
ACTCAGACAA TAGCACCAAG GCAGCGTGGG ACTCCATCCA GTCATTTCTG CAGTGTTGTG 540  
GTATAAATGG CACGAGTGAT TTGGACAGTG GCTCACCAGC ATCTTGCCCC TCAGATCGAA 600  
AAGTGGAGGG GTGCTATGCG AAAGAAGACT TTGGTTTCAT TCAATTTCTT GTATATCGGA 660  
ATCATCACCA TCTGTGTATG TGTGATTGAG GTGTTGGGGG ATGTCCTTTG CACTGACCCT 720  
GAACTGCCAG ATTGACAAAA CCAGCCAGAC CATAGGGGCTA TGATCTGCAG TAGTTCTGTG 780  
GTGAAGAGAC TTGTTTCATC TCCGGAAATG CAAAACCATT TATAGCATGA AGCCCTACAT 840  
GATCACTGCA GGATGATCCT CCTCCCATCC TTTCCCTTTT TAGGTCCCTG TCTTATACAA 900  
CCAGAGAAAGT GGGTGTGGC CAGGCACATC CCATCTCAGG CAGCAAGACA ATCTTTCACT 960  
CACTGACGGC AGCAGCCATG TCTCTCAAAG TGGTGAAACT AATATCTGAG CATCTTTTAG 1020  
ACAAGAGAGG CAAAGACAAA CTGGATTAA TGGCCCAACA TCAAAGGGTG AACCCAGGAT 1080  
ATGAATTTTT GCATCTTCCC ATTGTGCAAT TAGTCTCCAG CCTCTAAATA ATGCCAGTC 1140  
TTCTCCCCAA AGTCAAGCAA GAGACTAGTT GAAGGGAGTT CTGGGGCCAG GCTCACTGGA 1200  
CCATTGTCAC AACCTCTGT TTCTCTTTGA CTAAGTGCCC TGGCTACAGG AATTACACAG 1260  
TTCTCTTTCT CCAAAGGGCA AGATCTCATT TCAATTTCTT TATTAGAGGG CTTATTGAT 1320  
GTGTTCTAAG TCTTCCAGA AAAAACTAT CCAGTGATTT ATATCCTGAT TTCAACCAGT 1380  
CACTTAGCTG ATAATCACAG TAAGAAGACT TCTGGTATTA TCTCTCTATC AGATAAGATT 1440  
TTGTTAATGT ACTATTTTAC TCTTCAATAA ATAAACAGT TTATTATCTC AAAAAAAAAA 1500  
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1529

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BEPINOT01
- (B) CLONE: 546656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80 :

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GCATCCCCGC TTCCGGGTTA GGCCGTTCTT GCGCGCCCCC TCCTCTCCTC CCTTCGGACC 60
CATAGATCTC AGGCTCGGCT CCGCGCCCGC CGCAGCCCAC TGTTGACCCG GCCCGTACTG 120
CGGCCCCGTG GCCACCATGT CCCTGCACGG CAAACGGAAG GAGATCTACA AGTATGAAGC 180
GCCCTGGACA GTCTACGCGA TGAAGTGGAG TGTGCGGCCC GATAAGCGCT TTCGCTTGGC 240
GCTGGGCAGC TTCGTGGAGG AGTACAACAA CAAGGTTTCT CTTGTTGGTT TAGATGAGGA 300
GAGTTCAGAG TTTATTTGCA GAAACACCTT TGACCACCCA TACCCACCA CAAAGCTCAT 360
GTGGATCCCT GACACAAAAG GCGTCTATCC AGACCTACTG GCAACAAGCG GTGACTATCT 420
CCGTGTGTGG AGGGTTGGTG AAACAGAGAC CAGGCTGGAG TGTTTGCTAA ACAATAATAA 480
GAACTCTGAT TTCTGTGCTC CCCTGACCTC CTTTGACTGG AATGAGGTGG ATCCTTATCT 540
TTTAGGTACC TCAAGCATTG ATACGACATG CACCATCTGG GGGCTGGAGA CAGGGCAGGT 600
GTTAGGGCGA GTGAATCTCG TGTCTGGCCA CGTGAAGACC CAGCTGATCG CCCATGACAA 660
AGAGGTCTAT GATATTGCAT TTAGCCGGGC CGGGGGTGGC AGGGACATGT TTGCTCTGT 720
GGGTGCTGAT GGCTCGGTGC GGATGTTTGA CCTCCGCCAT CTAGAACACA GCACCATCAT 780
TTACGAAGAC CCACAGCATC ACCCACTGCT TCGCCTCTGC TGGAACAAGC AGGACCCTAA 840
CTACCTGGCC ACCATGGCCA TGGATGGAAT GGAGGTGGTG ATTCTAGATG TCCGGGTTCC 900
CTGCACACCT GTCGCCAGGT TAAACAACCA TCGAGCATGT GTCAATGGCA TTGCTTGGGC 960
CCCACATTCA TCCTGCCACA TCTGCACTGC AGCGGATGAC CACCAGGCTC TCATCTGGGA 1020
CATCCAGCAA ATGCCCCGAG CCATTGAGGA CCCTATCCTG GCCTACACAG CTGAAGGAGA 1080
GATCAACAAT GTGCAGTGGG CATCAACTCA GCGCGACTGG ATCGCCATCT GCTACAACAA 1140
CTGCCTGGAG AACTCAGAG TGTAGTGTG GTGGCGCTGT GCCACGAGG CAGGGGCTTT 1200
TGTATTTCTT GCCTCTGCCC CACCCCCAAA GTAAGAAGAA ACATGTTTCC AGTGGCCAGT 1260
ATGTCTTTCA TTGCTTTGCA CCCACTGTTA CCAGAAGCTG CTCTAGGAGT TCCTGGCCAG 1320

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TCACCCCATC GCCCTCTGTG GCAGACTCAG TGCTGTGTGG CGCCTCCTCA GCCCAGGGCT 1380  
GAGTTTTAAG ATTTTCTCTC CTTTCCTCTT CTCCTTTGGT TCCTCAATTA AAAAATGTGT 1440  
GTATATTTGT TTGTCAGGCG TTGTGTTGAG GAGCAGTTCA CGCACTGGCT GTGTCTATTC 1500  
CTCTGCCCAG GTGTCTCTGT TTGCTGCCCCA AGGCAGCAGT TCATGTCTCG TCCATGTCCA 1560  
TGTTTCGTGT AGCACTTACG TGGGAACAAA TACCAATTTG TCTTTTCTCC TAGTATCAGT 1620  
GTGTTTAACA AATTTTAACT TTGTATATTT GTTATCTATC AGGCTAATTT TTTTATGAAA 1680  
AGAATTTTAC TCTCCTGCTT CATTTCTTTG TCTTATAGTC CTCCCTCTTT GCACCTTCTT 1740  
CTCTTCCCTC AGTGCCTGGA GCTGGTACTG GGCCCTGGG CCCCATGAGC AGTTTGCCTT 1800  
CTTGAGTCAC TGCCTGTGTA GTACATACCT GACCGGGAGT CCAAACCACC TTGGTGCTCT 1860  
GAAGTCCACT GACTCATCAC ACCTTTCTTA GCCTGGCTCC TCTCAAGGGC ATTCTGGGCT 1920  
TGTAACAGA CATAGGAAGC CTCTGTTTAC CCTGAAGCAC CACTGTCCAG CCCATTGGTT 1980  
CCCCTGGCA GCATGGTAGA GCTGAGAGAA ACAGGCTCTC AGGGTACCTG ACTTGAGGGG 2040  
AATCGTTTCA TGAAGCTGAA CTTCAAGCAT ATTTCCAGTA CATTCTTTCA GAGTCTGTTT 2100  
TTCCATCCAA ATATAAGCCC CAGGCCATTC CACTTAGTGT CTTTTCAATG ATAGGCAAGA 2160  
ATGATATCTG AGTTGAACTT CGGTGCTTCT GTTGTTTGAG TTTACTGTGC CTGGTGGTAT 2220  
ATTGGGCATT CTTTGGATTG AGTGTTCTGA GGTGAGAGAG TCTTCCCGAG GCATCCTGTC 2280  
TGTGCTTCCA ACCCTGAACA AGACCTTACA TGAGAGATGG ACTGATGGAC TGCGGCAATC 2340  
CTGGGCTGTC AAGTGGATAG ATAGTTAAAA AGCATTATAC TGTGGGTAAT GAAAAGGGAG 2400  
GAAAAAAAAA GAAGGAAAAG GAATTATAGA CCCCCAGGGT CAGCCAGTTA AGAGCTCTAC 2460  
CCACACCTGT CAACCCCTCT CTCCCCCAGT TTAGGTTCTG AGCAGTATTG GACTTGTAGC 2520  
CTGCAGTTGT CTTTTGACTT GCAGGCCGCA GGTGTCTTTC TGTTATGTGA ATGAGTTCCA 2580  
TGGAGGGGCA TATGTGTGAT TCCACCGTTA GATGAGCCCT TGGGGCAGGC AGTTTGGGAT 2640  
GTGCTCTTGG GGGAAAGTTG GCTGTTTCCT TCGCTCTGC TCCTACCCGA AGGTTTTTAA 2700  
GTCCCTCTGA ATTGCTCATC TGAGATTAGT AGAGTAGCAG GCCTGAAGGA TGATGGTTTT 2760  
GTCCTCTTTG GTTCTCACCT GCTTGAGAAG TAAAACAGTA ACTTTGTTCT TCTGGGCCCT 2820  
TAAGCTTTTT TGTTAAGTC TTCCTTTTCA GAAGTAGATG TCATTATATG CCAAAGTCT 2880  
AGCTCTTTC TTTACCATAC AGGGACCTGT CCCAAAGAAA AAGGCTCTTT TTTTAGCCAG 2940  
CATATTTCCC CTTCTACCCT TTTACTTTGT TGTTCTGATT TTAGGACTCT GGCTGGCCAT 3000  
GTGCTTGTGG TTGCCTCTCC TGCATTTGCC ACTGGATTTG CACTGCATCG TTTGGAGATA 3060  
CAAAGCGAGC AGTTCTTGGT CAGAACCCTC CTCTGCTTTT CATTGTGTTT GATAATGGTT 3120  
ACTGGGTCCT TCTCTCAAGG GTAGCAAGGC CAAGCTGATG GCTGCTTGTT TAGGAGGCCA 3180

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TCAGTTCCTT CCTGTGGAGA AGGGTCTGAA ATGGAAGTCA GTGGTAGAAG GGGCTGGTCT 3240  
GCTGGGCAGG GCTTACATCC ACTGAGTTCT AAGATTCCTT TCCTGATCTG CACCTACGCC 3300  
TGGTCTGTAT GGTGGAATTT GTCAGCTGGA ACTCAGAAAC AACAACTGA AAAAAAATA 3360  
ATAATTAGAA CATATTTGCA TAAGATAGCT ATTTACTCTG GAAACCAACA ACTTTTGAGA 3420  
TTTCCCTTGC CCTGTGGACG CCCAGCTCCT GTCATCCTTC CTTAGGTCCT GCAGTACAGT 3480  
CTTCCCCTGA ATGCCACCGG GGACCCAGGG GGA CTCCACC CCCCTAAGCA AGCACACACA 3540  
TACTCACAGT TGATGAGTTG CTGGTCTTTG AGTCCCAGCT CTCTTACCCT CCCTTTACTC 3600  
CACCAGCCCG ACGACCCATG ACTGAGGAGG GGATTTCTAC AGTCTCAGGA TTTAGAAAGT 3660  
CTGTAAGCCA TCCATGCTCC AGAAAGCACC GATCTGTTGT AGTTGCAAAA ACAACTCTGT 3720  
AATTTGTTGA GGTTCCTCAA CTGACAGCCA GCGAGACTGG GTGGGAGGCC CTGGATCTGT 3780  
TCTCCCTGAC TGC GGGAGGA GCAGCCACTA GGACTTTAGC AGGAAGCCCA CATGGAGGCT 3840  
CCGCCAGGCT GTGGCCAGC TGGTGATGGC CCTTTTGCTC CTGGCAGCCT GAGGCACAGC 3900  
TGCCTGTATT GTCCTCATCT GTTCTGACTG AAGGATGGAG GTGCTGAATA AATTAGGCCT 3960  
CAGGCCTCTA CCACCAGAGA GCTGGAGAAT GGGTCCACGT CATTCAAGGA CCTGAATTTT 4020  
TTATGCTCAG GAGCATTGGA ATCCTCTTCT TCCAGGGAGG AATTAGCCTG CAAGGTTAGG 4080  
ACTTGAAGAG GGAAGGTATT TAATAACTGG GCGAGGATGG GTGTGGTGGC TCACACCTGT 4140  
AATCCCAGCA TTTTGGGAGG CTGAGGTGGC CAGATCCCAA GGTCAGAAGA TCGAGACCAT 4200  
CCTGGCTAAC ATGGTGAAAC CCCATCTCTA CTAAAAATAC AAAAAAAAT TAGCCGGGGG 4260  
TGGTGGCGGG TACCTGTAGT CCTAGCTACT TGGGAGGCTG AGGCAGGAGA ATGGCGTGAA 4320  
CCTGGGAGGT GGAGCTTGCA GTGAGCCAAG ATCGTCCACT CACTGCAGCC TGGCGACAGA 4380  
GCAAGCG 4387

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SYNORAT03
- (B) CLONE: 693453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81 :

GCCTGAGCGG GAAGCATTGG CGTCCGAGCG ACTTCTAGGA GCCTGGGGTT CGGCGCTATG 60



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GAGGAGCTCG ATGGCGAGCC AACAGTCACT TTGATTCCAG GCGTGAATTC CAAGAAGAAC 120  
CAAATGTATT TTGACTGGGG TCCAGGGGAG ATGCTGGTAT GTGAAACCTC CTTCAACAAA 180  
AAAGAAAAAT CAGAGATGGT GCCAAGTTGC CCCTTTATCT ATATCATCCG TAAGGATGTA 240  
GATGTTTACT CTCAAATCTT GAGAAAACCTC TTCAATGAAT CCCATGGAAT CTTTCTGGGC 300  
CTCCAGAGAA TTGACGAAGA GTTGAAGTGA AAATCCAGAA AATCTCAATT GGTTCGAGTG 360  
AGTAAAAACT ACCGATCAGT CATCAGAGCA TGTATGGAGG AAATGCACCA GGTTCGAATT 420  
GCTGCTAAAG ATCCAGCCAA TGGCCGCCAG TTCAGCAGCC AGGTCTCCAT TTTGTACGCA 480  
ATGGAGCTCA TCTGGAACCT GTGTGAGATT CTTTTTATTG AAGTGGCCCC AGCTGGCCCT 540  
CTCCTCCTCC ATCTCCTTGA CTGGGTCCGG CTCCATGTGT GCGAGGTGGA CAGTTTGTCTG 600  
GCAGATGTTT TGGGCAGTGA GAATCCAAGC AAACATGACA GCTTCTGGAA CTTGGTGACC 660  
ATCTTGGTGC TGCAGGGCCG GCTGGATGAG GCCCGACAGA TGCTCTCCAA GGAAGCCGAT 720  
GCCAGCCCCG CCTCTGCAGG CATATGCCGA ATCATGGGGG ACCTGATGAG GACAATGCCC 780  
ATTCTTAGTC CTGGGAACAC CCAGACACTG ACAGAGCTGG AGCTGAAGTG GCAGCACTGG 840  
CACGAGGAAT GTGAGCGGTA CCTCCAGGAC AGCACATTCG CCACCAGCCC TCACCTGGAG 900  
TCTCTCTTGA AGATTATGCT GGGAGACGAA GCTGCCTTGT TAGAGCAGAA GGAACCTCTG 960  
AGTAATTGGT ATCATTTTCT AGTGAAGCTG CTCTTGTACT CCAATCCCAC AGTAAAACCC 1020  
ATTGATCTGC ACTACTATGC CCAGTCCAGC CTGGACCTGT TTCTGGGAGG TGAGAGCAGC 1080  
CCAGAACCCC TGGACAACAT CTTGTTGGCA GCCTTTGAGT TTGACATCCA TCAAGTAATC 1140  
AAAGAGTGCA GCATCGCCCT GAGCAACTGG TGGTTTGTGG CCCACCTGAC AGACCTGCTG 1200  
GACCACTGCA AGCTCCTCCA GTCACACAAC CTCTATTTCT GTTCCAACAT GAGAGAGTTC 1260  
CTCCTGCTGG AGTACGCCTC GGGACTGTTT GCTCATCCCA GCCTGTGGCA GCTGGGGGTC 1320  
GATTACTTTG ATTACTGCCC CGAGCTGGGC CGAGTCTCCC TGGAGCTGCA CATTGAGCGG 1380  
ATACCTCTGA ACACCGAGCA GAAAGCCCTG AAGGTGCTGC GGATCTGTGA GCAGCGGCAG 1440  
ATGACTGAAC AAGTTCGCAG CATTTGTAAG ATCTTAGCCA TGAAAGCCGT CCGCAACAAT 1500  
CGCCTGGGTT CTGCCCTCTC TTGGAGCATC CGTGCTAAGG ATGCCGCCTT TGCCACGCTC 1560  
GTGTCAGACA GGTTCCTCAG GGATTACTGT GAGCGAGGCT GCTTTTCTGA TTTGGATCTC 1620  
ATTGACAACC TGGGGCCAGC CATGATGCTC AGTGACCGAC TGACATTCCT GGGAAAGTAT 1680  
CGCGAGTTCC ACCGTATGTA CGGGGAGAAG CGTTTTGCCG ACGCAGCTTC TCTCCTTCTG 1740  
TCCTTGATGA CGTCTCGGAT TGCCCCTCGG TCTTTCTGGA TGAATCTGCT GACAGATGCC 1800  
TTGCCCCCTT TGGAACAGAA ACAGGTGATT TTCTCAGCAG AACAGACTTA TGAGTTGATG 1860  
CGGTGTCTGG AGGACTTGAC GTCAAGAAGA CCTGTGCATG GAGAATCTGA TACCGAGCAG 1920

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CTCCAGGATG ATGACATAGA GACCACCAAG GTGGAAATGC TGAGACTTTC TCTGGCACGA 1980  
AATCTTGCTC GGGCAATTAT AAGAGAAGGC TCACTGGAAG GTTCCTGAGA ACTGCTTCAA 2040  
TGTGGTATCT TTGTATGGCA ATGTATATAG ATTTTTTAAA AGAATAAATG TTGTTTGCAA 2100  
AAAAAAAAAA AAAAAAA 2117

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT03
- (B) CLONE: 866885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82 :

GGCGGGCGGA GTCTGCAGGA TGGCACCGGA CCCCTGGTTC TCCACATACG ATTCTACTTG 60  
TCAAATTGCC CAAGAAATTG CTGAGAAAAT TCAACAACGA AATCAATATG AAAGAAAAGG 120  
TGAAAAGGCA CCAAAGCTTA CCGTGACAAT CAGAGCTTTG TTGCAGAACC TGAAGGAAAA 180  
GATCGCCCTT TTGAAGGACT TATTGCTAAG AGCTGTGTCA ACACATCAGA TAACACAGCT 240  
TGAAGGGGAC CGAAGACAGA ACCTCTTGGA TGATCTTGTA ACTCGAGAGA GACTACTTCT 300  
GGCATCCTTT AAGAATGAGG GTGCCGAACC AGATCTAATC AGGTCCAGCC TGATGAGTGA 360  
AGAGGCTAAG CGAGGAGCAC CCAACCCTTG GCTCTTTGAG GAGCCAGAGG AGACCAGAGG 420  
CTTGGGTTTT GATGAAATCC GGCAACAGCA GCAGAAAATT ATCCAAGAAC AGGATGCAGG 480  
CCTTGATGCC CTTTCCTCTA TCATAAGTCG CCAAAAACAA ATGGGGCAGG AAATTGGGAA 540  
TGAATTGGAT GAACAAAATG AGATAATTGA CGACCTTGCC AACCTAGTGG AGAACACAGA 600  
TGAAAACTT CGCAATGAAA CCAGGCGGGT AAACATGGTG GACAGAAAGT CAGCCTCTTG 660  
TGGGATGATC ATGGTGATTT TACTGCTGCT TGTGGCTATC GTGGTTGTTG CAGTCTGGCC 720  
GACCAACTGA TGGCAGTAAA GAGACCACCA GCAGTGACAC CTGGCAATGA CAGATGCAAG 780  
CCCAACACCC TTTTGGTACG CAAACCTGC TCTCAATAAA TTCCCCAAA GCTCTGAAAA 840  
AAAAAA 846

(2) INFORMATION FOR SEQ ID NO: 83:

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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1011 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:  
(A) LIBRARY: LUNGNOT03  
(B) CLONE: 1242271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83 :

GAAAGAGATA ACTGGAAGTT CCTTGATTCA GAAAACAGAT TCAGATGAAG AAGTTGCAAT 60  
GCTGTTGGAC ACAGTCCAGA AAGTATTTCA GAAAATGTTG GAATGTATTG CACGGAGCTT 120  
CAGGAAGCAG CCGGAAGAAG GCCTGCGGCT GCTTTATTCT GTTCAGAGGC CTCTTCATGA 180  
GTTCACTACT GCTGTTCACT CTCGGCACAC AGACACCCCT GTGCACCGGG GTGTAATTTT 240  
TACTCTGATC GCTGGGCTTG TGGTTGAGAT AAGTCACCAG CTACGGAAGG TTTCTGACGT 300  
AGAAGAGCTT ACCCCTCCAG AGCATCTTTC TGATCTTCCA CCATTTTCAA GGTGTTTAAAT 360  
AGGAATAATA ATAAAGTCTT CGAATGTGGT CAGGTCATTT TTGGATGAAT TAAAGGCATG 420  
TGTGGCTTCT AATGATATTG AAGGCATTGT GTGCCTCACG GCTGCTGTGC ATATTATCCT 480  
GGTTATTAAT GCAGGTAAAC ATAAAAGCTC AAAAGTGAGG GAGGTTGCAG CCACTGTTCA 540  
CAGAAAACTA AAGACATTCA TGGAAATTAC TTTGGAAGAG GATAGCATTG AAAGATTTCT 600  
CTATGAATCA TCATCAAGAA CTCTGGGAGA ACTTTTGAAT TCATAACCAA GCCAACATCT 660  
CCAGACATGT AAAAATAGGG AAAAGTGATT CAAATTGAAA TGCCTGTGTA TTTTCCTATT 720  
GTTTTTAATG TTAATAACCC ATATAATAGG GAAAGGGTGG GATTTTTTTG TGGGAATGTG 780  
GGAAGGTGGG GGTATGAGAG GAGATAACTC AAAACTTCTT CAATTTTGCC TAGTGCCTGC 840  
GTAAATAATA TATTTAATAT AAAGGACTCC AGGTATGAAT GGTGTAGAAA TCCATGATTC 900  
CAAGAAAAAA CACTTTTCTA GCAAACCTGG TTGTTTTTAA AATGACTTTT ATATATGTAA 960  
TATTGCTTGG AACTATGAG TAATAAGCA ATGACAACAT CAAAAAAA A 1011

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2478 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:  
(A) LIBRARY: LUNGFET03  
(B) CLONE: 1255027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84 :

CCCACGCGTC CGCCACGCG TCCGCAGCGC TGTGTTTGCG AGCGGGAGCG AGGGGCGCCG 60  
 GCTGGGGTGT GTGCTCCTGA GCTCTTCAGA AACCAGGCTG CTTTCAGGAA CATTGCTGTG 120  
 GATTCCCAGC TTTCAGACAA CACATGACTA AGACAGATGA GACCACTCTA GTTGCCTCAT 180  
 GGGAAACTCG GGAAAAGACT GCAAAAACAA CATTGTTTCT CCCTTTGGAA TTCTGGAGTT 240  
 ATAAGGCAGA GGTCCCCCAT CTTCCCGAAC TGGCCTATTC CGCTAGAAGC AAGATGGCTG 300  
 AACTCAATAC TCATGTGAAT GTCAAGGAAA AGATCTATGC AGTTAGATCA GTTGTTCCCA 360  
 ACAAAAGCAA TAATGAAATA GTCCTGGTGC TCCAACAGTT TGATTTTAAT GTGGATAAAG 420  
 CCGTGCAAGC CTTTGTGGAT GGCAGTGCAA TTCAAGTTCT AAAAGAATGG AATATGACAG 480  
 GCAAAAAGAA GAACAATAAA AGAAAAAGAA GCAAGTCCAA GCAGCATCAA GGCAACAAAG 540  
 ATGCTAAAGA CAAGGTGGAG AGGCCTGAGG CAGGGCCCCT GCAGCCGCAG CCACCACAGA 600  
 TTCAAAACGG CCCCATGAAT GGCTGCGAGA AGGACAGCTC GTCCACAGAT TCTGCTAACG 660  
 AAAAACCAGC CTTATCCCT CGTGAGAAAA AGATCTCGAT ACTTGAGGAA CCTTCAAAGG 720  
 CACTTCGTGG GGTACAGAA GGCAACAGAC TACTGCAACA GAACTATCC TTAGATGGGA 780  
 ACCCCAAACC TATACATGGA ACAACAGAGA GGTGAGATGG CCTACAGTGG TCAGCTGAGC 840  
 AGCCTTGTA CCAGCAAG CCTAAGGCAA AAACATCTCC TGTTAAGTCC AATACCCTG 900  
 CAGCTCATCT TGAAATAAAG CCAGATGAGT TGGCAAAGAA AAGAGGCCCA AATATTGAGA 960  
 AATCAGTGAA GGATTGCAA CGCTGCACCG TTTCTCTAAC TAGATATCGC GTCATGATTA 1020  
 AGGAAGAAGT GGATAGTTCC GTGAAGAAGA TCAAAGCTGC CTTTGCTGAA TTACACAACT 1080  
 GCATCATTGA CAAAGAAGTT TCATTAATGG CAGAAATGGA TAAAGTTAAA GAAGAAGCCA 1140  
 TGGAAATCCT GACTGCTCGT CAGAAGAAAG CAGAAGAACT AAAGAGACTC ACTGACCTTG 1200  
 CCAGTCAGAT GGCAGAGATG CAGCTGGCCG AACTCAGGGC AGAAATTAAG CACTTTGTCA 1260  
 GCGAGCGTAA ATATGACGAG GAGCTCGGGA AAGCTGCCCCG GTTTTCCTGT GACATCGAAC 1320  
 AGCTGAAGGC CCAAATCATG CTCTGCGGAG AAATTACACA TCCAAAGAAC AACTATTCCT 1380  
 CAAGAACTCC CTGCAGCTCC CTGCTGCCTC TGCTGAATGC GCACGCAGCA ACCTCTGGGA 1440  
 AACAGAGTAA CTTTTCCCGA AAATCATCCA CTCACAATAA GCCCTCTGAA GGCAAAGCGG 1500  
 CAAACCCCAA AATGGTGAGC AGTCTCCCCA GCACCGCCGA CCCCTCTCAC CAGACCATGC 1560  
 CGGCCAACAA GCAGAATGGA TCTTCTAACC AAAGACGGAG ATTTAATCCA CAGTATCATA 1620  
 ACAACAGGCT AAATGGGCCT GCCAAGTCGC AGGGCAGTGG GAATGAAGCC GAGCCACTGG 1680  
 GAAAGGGCAA CAGCCGCCAC GAACACAGAA GACAGCCGCA CAACGGCTTC CGGCCCAAAA 1740  
 ACAAAGGCGG TGCCAAAAAT CAAGAGGCTT CCTTGGGGAT GAAGACCCC GAGGCCCCCG 1800

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CCCATTCTGA AAAGCCCCGG CGAAGGCAGC ACGCTGCAGA CACCTCGGAG GCCAGGCCCT 1860  
TCCGGGGTAG TGTCGGTAGG GTTTCACAGT GCAATCTCTG CCCCACGAGA ATAGAAGTTT 1920  
CCACAGATGC AGCAGTTCTC TCAGTCCCGG CTGTGACGTT GGTGGCCTGA GCTAGGAGGA 1980  
AAAAGAGCAG TTTTCACTCA GTTTTGGTTC CCTGCCCAGG GTGCTGACCC AATTCGCTGC 2040  
CAAAAGAGTG TCAATCAGAA TATACAAATC CCGTATGGTT GTGTCATCCT CTCTTAATCA 2100  
TTTTTACTAA TTCTAATAAT CAGCTCTAGC TTGCTTCATA ATTTTCATGG CTTTGCTTGA 2160  
TCTGTTGATG CTTTCTCTCA TCAAGACTTT GCAGCATTTT AGCCAGGCAG TATTTACTCA 2220  
TTATTAGGAA AATCAAGATG TGGCTGAAGA TCAGAGGCTC AGTTAGCAAC CTGTGTTGTA 2280  
GCAGTGATGT CAGTCCATTG ATTGTCTTTA GAGAGTTAAT GTTACAAAAA AGAATTCTTA 2340  
ATAATCAGAC AAACATGATC TGCTGAGGAC ACATGCGCTT TTGTAGAATT TAACATCTGG 2400  
TGTTTTTCTG AAAAAATATA TATACATATA TTGCTTTATT TGAAACAAAT TAAATATATGC 2460  
TGCATTTGAA AAAAAAAA 2478

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TESTTUT02
- (B) CLONE: 1273453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85 :

TGCACATCTA GCACAAATTG AAGATGATAG AGCTGCGATG GTTATTTCTT GGCATCTGGC 60  
AAGTGACATG GACTGTGTAG TCACCCTAAC CACTGACGCT GCACGTCGTA TCTATGATGA 120  
AACCCAAGGT CGTCAGCAGG TGTTGCCCCCT TGATTCTATT TACAAGAAGA CTCTTCCAGA 180  
TTGGAAAAGA TCTCTACCTC ATTTCCGAAA TGGAAAATTG TATTTTAAAC CCATTGGAGA 240  
TCCAGTCTTT GCTCGAGACT TGTTAACATT TCCAGATAAT GTAGAACATT GTGAAACAGT 300  
ATTTGGTATG CTGTTAGGAG ACACCATTAT TTTGGATAAT CTGGATGCGG CCAATCATT 360  
TAGAAAAGAG GTTGTAAAAA TTACACACTG TCCTACACTG CTGACCAGAG ATGGAGATCG 420  
AATTCGAAGT AATGGAAAGT TTGGGGGCCT TCAGAATAAA GCTCCTCAA TGGATAAACT 480  
TCGGGGAATG GTATTTGGAG CTCCAGTTCC AAAACAGTGT CTGATCTTAG GGGAACAAAT 540  
AGATCTTCTT CAGCAGTATC GTTCTGCTGT GTGCAAACTA GACAGTGTGA ATAAGGATCT 600

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TAACAGTCAA TTAGAGTACC TTCGCACTCC GGATATGAGG AAGAAAAAGC AAGAACTTGA 660  
TGAACATGAG AAAAATCTCA AACTAATAGA GGAAAAACTA GGTATGACTC CCATACGTAA 720  
GTGTAATGAC TCATTGCGTC ATTCACCAAA GGTGAGACG ACAGATTGTC CAGTTCCTCC 780  
TAAAAGAATG AGACGAGAAG CTACAAGACA AAATAGGATT ATAACCAAAA CAGATGTATG 840  
AGAGGTGACA GAGAGAAGAG GCCATTGGTC TCAGTAAGAA TGCCCTGCTT TCTGCATCTC 900  
TGTTTCAGAA GACCAAGAGG GTGACTTACC AGACTGAGTA TTTCTGGGGA CAATACAAGT 960  
ACCTGGGCAT GAATTTCCAT TTCGATTGAG ATGGGACTGG AAACAACCAT TCAATTTTAT 1020  
GAATCTTACT GGACATTATG GATTTACTGG AATTATTCCA GACATTATGC CCTTTGGTTG 1080  
TCACTACCTT GCAAATGTGT AAGAGGAAAA TGTGCTAATG TGGCAGTGAC TGTAAAACTG 1140  
GCACATGGCA TTTATTAATC CTGAAGAAAA GTACATGTAC TATTTTTCAG TATAAATATA 1200  
ATGAACATGT CAGAACTATT TCTTGAAAAC CTTTTTATTA CTTTTCGCTG AATTTATTTA 1260  
ACAAAGATGT TTTGTCTTTT GTGTAAGGGA GGTCTAGAG GCTAGATGTT TAATTGTAAA 1320  
TATGTGAGGA AACTCAATGC AGAATTCAGG ATAAAAATTT TAAAAGCACA GGTATTTGGG 1380  
AATTGAAATG TTAAGATACC CAGAACAACA TTAAATCAAT GAGTGAACCT GTGACAGTGG 1440  
TAGCATTTCA AATTTCAAAA GACTTATCCT GTGTGTGTGT GTGTGTGTGT ATATATATAT 1500  
ATATATATAT AAATATATAT ATATAAATA TTCAGCAGCA CCAAGTTTTA TAACTATTGT 1560  
TTGTTTGAAT TTATTAATAC TAGAATATGT AGTCTCAGCC TTAATTTTAC ATTTACATTA 1620  
TTTTGTAATT TTTTATTACT ATTTTAAAGG GGTTAAAGAG AACATACATT CTCACATTAG 1680  
TGTAATTTCT GGTAGAAAGT TGCTGCAAAA ACATTTGAAA TGTATATTAA CCTAATGTAT 1740  
GTCATATATA TGTCTTTGTG TAAGTTCAAG ACTATTGATC TGTGAAGTTA TTTTGTAAGG 1800  
ACATACATTT GGTAAGTAAG TTTGTGTCCC AGGAAATGTA TGTGTTTTTA AACCCCTTCT 1860  
AAATATGCAG GCCATTAATA AATAAGATTG TGTCTCA 1897

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TESTTUT02
- (B) CLONE: 1275261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86 :

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CCCACGCGTC CGGGGACATC CTGTTCTGAG TCAAGATTCC TCCTTCTGAA CATGGGACTT 60  
TCCAGAAGGA CCACAGCTCC TCCCGTGCAT CCACTCGGCC TGGGAGGTTT TGGATTTTGG 120  
CTGTCGAGGG AGTTTGCCTG CCTCTCCAGA GAAAGATGGT CATGAGGCCC CTGTGGAGTC 180  
TGCTTCTCTG GGAAGCCCTA CTTCCCATTA CAGTTACTGG TGCCCAAGTG CTGAGCAAAG 240  
TCGGGGGCTC GGTGCTGCTG GTGGCAGCGC GTCCCCCTGG CTTCCAAGTC CGTGAGGCTA 300  
TCTGGCGATC TCTCTGGCCT TCAGAAGAGC TCCTGGCCAC GTTTTTCCGA GGCTCCCTGG 360  
AGACTCTGTA CCATTCCCGC TTCCTGGGCC GAGCCCAGCT ACACAGCAAC CTCAGCCTGG 420  
AGCTCGGGCC GCTGGAGTCT GGAGACAGCG GCAACTTCTC CGTGTGATG GTGGACACAA 480  
GGGGCCAGCC CTGGACCCAG ACCCTCCAGC TCAAGGTGTA CGATGCAGTG CCCAGGCCCCG 540  
TGGTACAAGT GTTCATTGCT GTAGAAAGGG ATGCTCAGCC CTCCAAGACC TGCCAGGTTT 600  
TCTTGTCTG TTGGGCCCCC AACATCAGCG AAATAACCTA TAGCTGGCGA CGGGAGACAA 660  
CCATGGACTT TGGTATGGAA CCACACAGCC TCTTCACAGA CGGACAGGTG CTGAGCATTT 720  
CCCTGGGACC AGGAGACAGA GATGTGGCCT ATTCTGCAT TGTCTCCAAC CCTGTCAGCT 780  
GGGACTTGGC CACAGTCACG CCCTGGGATA GCTGTCATCA TGAGGCAGCA CCAGGGAAGG 840  
CCTCCTACAA AGATGTGCTG CTGGTGGTGG TGCCTGTCTC GCTGCTCCTG ATGCTGGTTA 900  
CTCTCTTCTC TGCCTGGCAC TGGTGCCCTT GCTCAGGGAA AAAGAAAAAG GATGTCCATG 960  
CTGACAGAGT GGGTCCAGAG ACAGAGAACC CCCTTGTGCA GGATCTGCCA TAAAGGACAA 1020  
TATGAACTGA TGCCTGGACT ATCAGTAACC CCACTGCACA GGCACACGAT GCTCTGGGAC 1080  
ATAACTGGTG CCTGGAAATC ACCATGGTCC TCATATCTCC CATGGGAATC CTGTCCTGCC 1140  
TCGAAGGAGC AGCCTGGGCA GCCATCACAC CACGAGGACA GGAAGCACCA GCACGTTTCA 1200  
CACCTCCCCC TTCCCTCTCC CATCTTCTCA TATCCTGGCT CTTCTCTGGG CAAGATGAGC 1260  
CAAGCAGAAC ATTCCATCCA GGACACTGGA AGTTCTCCAG GATCCAGATC CATGGGGACA 1320  
TTAATAGTCC AAGGCATTCC CTCCCCACC ACTATTCTA AAGTACTAAC CAACTGGCAC 1380  
CAAGAAAAAA TCCTCACTAA CCGCATCATC CGACAATAA TAATTCACAC TACATCCAAA 1440  
CATCACTTAG GCGGCGGGGC CGCCGACTGG TTCCGGGCTT AGGGTGGG 1488

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: COLNNOT16  
(B) CLONE: 1281682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87 :

CCGACTTTGT AGCATTTTTTA TTTAAGCTAA AACAGAGCAC ATGTATATGT ACATAAGACA 60  
CATTAAATCT ATAAATACTA TTTATTTCATT TTATATAAAC TAATGTAATG GAAAACAAAT 120  
TCTTATGACT TTGTGGTTTT ATAGATGTTT TAGAAACTTT GTATGTAGGT ATCTACAAAA 180  
TTAGTTCATT CCCCTGAATA TTTTTCATT CATATTTTTG AGGTCTTGAT GTTTTCAGCC 240  
TCTGGCGAAT CTTTTTCATT GAATTTGAAC CATTTGTAAA ATCTGTGATG CTGAAGCAGA 300  
GTGTGTCACA AAGTGATGAG AACATTACTA AAATCCACGG ACGCACTGCG ACCTAAGGGC 360  
TCAACGGCTG ACTCGGCAGC GGGCAGCCAC CCCACGCTCC CCTGCGGTCA CTCGCACACC 420  
ACAGCCTGAA GCTCCCCCAG CGCCTGCACC TCGCACACAG CTAAGGTCAA AGTTCAAACG 480  
CACTCCACAC GGAAGCTCAT TCTATACCCG AAGAGCAGTC TCAGAAAGCA AGATTACTTT 540  
TGTGTTTTTT AAAAAATGAT TCTTTAATGT ATTTTCTAA ACATTCTGAT TGGAAGTAGT 600  
GGATTCCTAA ATGATTCCAA AGTCATCTGT AATTCTTCTG TTTTGTGTTT GTTCTGTCTT 660  
TTCTTCATTT TGGCTTTGGG TGGGGGGAGG GGCAGGTGAC ACAAAGGATT TTTTTTTTTT 720  
TTTTTTTTTA ATTTTGGAA TCTTTTCCAA TAACCAGCTA AAGATTGCA CTGAAATACA 780  
ACTTGTATGC CTTTTGCATT TTTAAGCCT GCTTCCTGGA TTTAAGCAGA GTGATAGTGT 840  
TCAAAGAGCC AGTTCAGCCT GTAACATATT TGAAAAAGAT ATGTCTGCAC TTTGAGGTCC 900  
CTTTTGAATG CCATTCACTA GACCTCTCAA GCATTTTGTT TCATTGCTAC ATCCAAGCGC 960  
CTCACAAGTC CACAATGCGG GACAGCATCA AAAGCTCAAG ACTTTGGAAA AAGCTTGTGG 1020  
GCTTGCACTG GGGGAGGGAA GGGAACAAAA TTTGTGTACT TCTTTGTTTA ATTTAGAAAT 1080  
AAGGCATCCA AGAGATGCCA TTATTTTCTG TGTTTCAATT GTTGTGCCTT TGAGTTAAAC 1140  
TGCATTTTTG TCTTTTGTT GAAATCTGAA ATGTACTGTC CCAATATAAA ACAGTAATTA 1200  
TTTGACCTTT GCACTGTTT TCTGGTCCTT TTCAGTTTGA TTGCATATAA ATGTGGAAC 1260  
TGATAGATCT CTATATTTTT AATGCACTTG TGATAAACTG GCAGCAGGGT TAGACATTAC 1320  
TTTCAAAGCT TGAGGTAGAC CGAGTCAGCA TGCTAGA 1357

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2330 base pairs  
(B) TYPE: nucleic acid



(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: BRSTNOT07  
(B) CLONE: 1298305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88 :

CCTACTTGTT CCCACCTTGG GAGAGGACGA TGA CT TGGA GGGACGCGTG AAGGGAGAAG 60  
GGGTCCCTCCC ATGAGGCTGA GGATGGCCTG AACCTGGAGC AGCGGACCAG GCAGACGGGC 120  
TGAAGTGGGG TCCCAAATTC CATGTCCAGA GGTGTGGGGA GCCTGCCTCC CTAGCTCCTG 180  
GCCCCTGCCA GGGGCTTACA TCAAAACACC TCAGAGGGCT GCCCTCCAGA GGCTGCACCC 240  
AGAACAGTGG GACATGAGCA GGGGTGTGGG CTTGGAGGGT GAAGAGGATG TGGTCCTATC 300  
AGATGCTGGG CCTCCTCAGC CATAGCCCCC TGCTCCTACC CCCTGACTGG CTCTTGCTGTC 360  
CTCACCTCTC ACCCTCTCCT TCCTGGGAGG CCCTGGGAGG TGATCATTGA CACCCAGCCA 420  
AGCAGACAGC TGCGGGTGCC CAAGCCCTTG CTGGGCCTGC GCGTGAGGAG TCCCACTGCT 480  
TCTAAAGGAA GTCCTGGGCA GGAGGTGGCT TTGGTGGTTG GTTCCAAAGT TGAAAATGCT 540  
TGCAGTTTGA CCTTAGAAGA AGTGGGAAGA AGAAGGAGCT CTACAGGGTC AGCTTTGTTT 600  
GATTTGTCCA GTCTAAGAAG TCCCAT TGCC AAAGCTTTCT GCAGGAGGGT GAATGCCGCA 660  
GCTTGGCAGC CCCTGGGTTT CTCTTGAAA TGGTCAGTTT CCCCTCAAAG TACCCAAAGT 720  
AGCCTTGCTG TGAGTTTTTG TCCTTGCTC CTTTTTAGAG AAGAGGGCAT TTAGACTGCA 780  
TTTTCTGCT TAAAGAAGGT TAAAGCAAAT GTTTATTGCC TTTTCTAGTG AACTAACTCG 840  
TAGAGATGTT CTCAGCAGGA AGACAGTCTT AGCACTGTCA CTTAGCAGAT TGCACTTAAG 900  
TCCCTTGCTG TGGCCAGATG GCGTGGCTGG TTGCCTTAAT ATGTCCCAGG ACCCCTGACA 960  
GGGCTGCCTG GCCTCTCCCT CGTGCTCCTC AAGAGCCCAG TCCATACACT GTGGATGTCA 1020  
TTGCTGTCGG GTTAGGAAGT CTTGTCTTAG AACGCCCTGG CTGGTATGAC CACAGTTCAT 1080  
GGCGGCTCTT CTCGCTTGGG TCATGGTCAT CTTCCAGCAC CTGCTGTGCT GGAAGGCCG 1140  
AGGATGGGGG CCCAGCACTG TCCAGGCCTG CTGGGGCCTG GCTGGGAGTC CTGTGGGCAG 1200  
CATGGAACAT GCAGCTGGGC TTCCTGTGAC CAGGCACCCT CTGGCACTGT TGCTTGCCCT 1260  
GTGCCCTGGA CCTTTTCTG CCCTTCTCCT TCCTCTGCTC CCTTGGGGCT ACCCCTTGCC 1320  
CCCTCCTGGT CTGTGCAAAC TCCCTCAGGG AGCCCCCTG CCCTGTAGCT CTCCTTAAC 1380  
TTCCTAGGGG CTGCTGAGCC CACCCAGAGG TTGTTGGAGT TCAGCGGGGC AGCTTGCTCTC 1440  
CCTTGTCAGC AGGGGCGTAA GGGCTGGGTT TGGCCATACA AGGTTGGCTA CGCCCTCAAT 1500  
CCCTGACCGT TCCAGGCACT GAGCTGGGCA CCCACGGAAG GACATGCTGT CCAGACTGTG 1560

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ATGACTGCCA GCACAGGGCA TCTCGGGCTT GGCTGGTCTG CGAGGCCTTG CCCCTGTGGA 1620  
ACTCTGGGTT CCTGTTTTCT CAGTCTTTTT GCGGCTTTGC TGTGGTTGGC AGCTGCCGTA 1680  
CTCCAGGCTT GTGTCGGCCA CTCAGATGAG GGCTGTGGTG CGAGCCAGTG CAGGAGAGCT 1740  
GCGCTTGGGA TTGTGCCCTC TCCTGTGTCT GTCCTCCGGA CCTACCCAGG TCTCCACCAT 1800  
CAGGACCCTG TCTTTGGGTT TAGAAGACCA AGTATGGGGA AAACCAGACA CCAGCCTCTG 1860  
CAGCAATGGG TCCCTCTAGC CTGTGGACAC CAGCTGGGGG ATCCAGGGTC AGGCCCCCTC 1920  
CTCTCCCCAG TTTCCCTCTG CTGTGGGTTT TGGGCTGTCA TGTCTCCACC ACTTAAGGAT 1980  
GTCTTTACAC TGAATTCAGG ATAGATGCTG GGATGCCTGG GCATGGCCAC ATGTTACATG 2040  
TACAGAACTT TGTCTACAGC ACAAATTAAG TTATATAAAC ACAGTGAAGT GTATTTAATG 2100  
CTGATCTACT ATAAGGTATT CTATATTTAT ATGACTTCAG AGACGCGTAT GTAATAAAGG 2160  
ACGCCCTCCC TCCAGTGTCC ACATCCAGTT CACCCCAGAG GGTCGGGCAG GTTGACATAT 2220  
TTATTTTTGT CTATTCTGTA GGCTTCCATG TCCAGAATCC TGCTTAAGGT TTTAGGGTAC 2280  
CTTCAGTACT TTTTGCAATA AAAGTATTTT CTATCCAAAA AAAAAAAAAA 2330

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGNOT12
- (B) CLONE: 1360501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89 :

CTACACCTTT TCCATTTGCT AATAAGGCCC TGCCAGGCTG GGAGGGAATT GTCCCTGCCT 60  
GCTTCTGGAG AAAGAAGATA TTGACACCAT CTACGGGCAC CATGGAAGT CTTCAAGTGA 120  
CCATTCTTTT TCTTCTGCCC AGTATTTGCA GCAGTAACAG CACAGGTGTT TTAGAGGCAG 180  
CTAATAATTC ACTTGTTGTT ACTACAACAA AACCATCTAT AACAACACCA AACACAGAAT 240  
CATTACAGAA AAATGTTGTC ACACCAACAA CTGGAACAAC TCCTAAAGGA ACAATCACCA 300  
ATGAATTACT TAAAATGTCT CTGATGTCAA CAGCTACTTT TTTAACAAGT AAAGATGAAG 360  
GATTGAAAGC CACAACCACT GATGTCAGGA AGAATGACTC CATCATTTCA AACGTAACAG 420  
TAACAAGTGT TACACTTCCA AATGCTGTTT CAACATTACA AAGTTCCAAA CCCAAGACTG 480  
AAACTCAGAG TTCAATTAAA ACAACAGAAA TACCAGGTAG TGTTCTACAA CCAGATGCAT 540

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CACCTTCTAA AACTGGTACA TTAACCTCAA TACCAGTTAC AATTCCAGAA AACACCTCAC 600  
AGTCTCAAGT AATAGGCACT GAGGGTGGAA AAAATGCAAG CACTTCAGCA ACCAGCCGGT 660  
CTTATTCCAG TATTATTTTG CCGGTGGTTA TTGCTTTGAT TGTAATAACA CTTTCAGTAT 720  
TTGTTCTGGT GGGTTTGTAC CGAATGTGCT GGAAGGCAGA TCCGGGCACA CCAGAAAATG 780  
GAAATGATCA ACCTCAGTCT GATAAAGAGA GCGTGAAGCT TCTTACCGTT AAGACAATTT 840  
CTCATGAGTC TGGTGAGCAC TCTGCACAAG GAAAAACCAA GAACTGACAG CTTGAGGAAT 900  
TCTCTCCACA CCTAGGCAAT AATTACGCTT AATCTTCAGC TTCTATGCAC CAAGCGTGGA 960  
AAAGGAGAAA GTCCTGCAGA ATCAATCCCG ACTTCCATAC CTGCTGCTGG ACTGTACCAG 1020  
ACGTCTGTCC CAGTAAAGTG ATGTCCAGCT GACATGCAAT AATTTGATGG AATCAAAAAG 1080  
AACCCCGGGG CTCTCCTGTT CTCTCACATT TAAAAATTCC ATTACTCCAT TTACAGGAGC 1140  
GTTCCTAGGA AAAGGAATTT TAGGAGGAGA ATTTGTGAGC AGTGAATCTG ACAGCCCAGG 1200  
AGGTGGGCTC GCTGATAGGC ATGACTTTCC TTAATGTTTA AAGTTTTCCG GGCCAAGAAT 1260  
TTTTATCCAT GAAGACTTTC CTACTTTTCT CCGTGTTCTT ATATTACCTA CTGTTAGTAT 1320  
TTATTGTTTA CCACTATGTT AATGCAGGGA AAAGTTGCAC GTGTATTATT AAATATTAGG 1380  
TAGAAATCAT ACCATGCTAC TTTGTACATA TAAGTATTTT ATTCCTGCTT TCGTGTTACT 1440  
TTAATAAAT AACTACTGTA CTCAATACTC TAAAAATACT ATAACATGAC TGTGAAAATG 1500  
GCAATGTTAT TGTCTTCCTA TAATTATGAA TATTTTTGGA TGGATTATTA GAATACATGA 1560  
ACTCACTAAT GAAAGGCATT TGTAATAAGT CAGAAAGGGA CATAGGATTC ACATATCAGA 1620  
CTGTTAGGGG GAGAGTAATT TATCAGTTCT TTGGTCTTTC TATTTGTCAT TCATACTATG 1680  
TGATGAAGAT GTAAGTGCAA GGGCATTAT AACACTATAC TGCATTCAAT AAGATAATAG 1740  
GATCATGATT TTTCATTAAC TCATTTGATT GATATTATCT CCATGCATTT TTTATTTCTT 1800  
TTAGAAATGT AATTATTTGT TCTAGCAATC ATTGCTAACC TCTAGTTTGT AGAAAATCAA 1860  
CACTTTATAA ATACATAATT ATGATATTAT TTTTCATTGT ATCACTGTTC TAAAAATACC 1920  
ATATGATTAT AGCTGCCACT CCATCAGGAG CAAATTCTTC TGTTAAAAGC TAACTGATCA 1980  
ACCTTGACCA CTTTTTTGAC ATGTGAGATC AAAGTGTCOA GTTGGCTGAG GTTTTTTGGG 2040  
AAGCTTTAGA ACTAATAAGC TGCTGGTGGC AGCTTTGTAA CGTATGATTA TCTAAGCTGA 2100  
TTTTGATGCT AAATTATCTT AGTGATCTAA GGGGCAGTTT AGTGAAGATG GAATCTTGTA 2160  
TTTAAAATAG CCTTTTAAAA TTTGTTTTGT GGTGATGTAT TTTGACAACT TCCATCTTTA 2220  
GGAGTTATAT AATCACCTTG ATTTTAGTTT CCTGATGTTT GGACTATTTA TAATCAAGGA 2280  
CACCAAGCAA GCATAAGCAT ATCTATATTT CTGACTGGTG TCTCTTTGAG AAGGATGGGA 2340  
AGTAGAAAAA AAAAAAAGAA AGAAAGGAAA GGAAGAGAGG AGAGAAGAAG GCAGGGATCT 2400

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CCACTATGTA TGTTTTCACT TTAGAACTGT TGAGCCCATG CTTAATTTTA ATCTAGAAGT 2460  
CTTTAAATGG TGAGACAGTG ACTGGAGCAT GCCAATCAGA GAGCATTGT CTTCAGAAAA 2520  
AAAAAAAATC TGAGTTTGAG ACTAGCCTGG CCAACATGTT GAAACCCCAT ATCTACTAAA 2580  
AATACAAAAA TTAGCCTGGT GTGGTGGCGC ACGCCTGTAG TCCCAGCTAC TCTGGAGCCT 2640  
GAGGAACGTG AATCGCTTGA ACCCAGAAGA CAGAGGTTGC AGTGAGCTGA GATGGCACTA 2700  
TTGCACTCCA GACTGGTGAC ACACGCAGA 2729

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGNOT12
- (B) CLONE: 1362406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90 :

GGCCCCTGCA CTGCTCCTGA TCCCTGCTGC CCTCGCCTCT TTCATCCTGG CCTTTGGCAC 60  
CGGAGTGGAG TTCGTGCGCT TTACCTCCCT TCGGCCACTT CTTGGAGGGA TCCCGGAGTC 120  
TGGTGGTCCG GATGCCCCGCC AGGGATGGCT GGCTGCCCTG CAGACCGCAG CATCCTTGCC 180  
CCCCTGGCAT GGGATCTGGG GCTCCTGCTT CTATTTGTTG GGCAGCACAG CCTCATGGCA 240  
GCTGAAAGAG TGAAGGCATG GACATCCCGG TACTTTGGGG TCCTTCAGAG GTCACTGTAT 300  
GTGGCCTGCA CTGCCCTGGC CTTGCAGCTG GTGATGCGGT ACTGGGAGCC CATACCCAAA 360  
GGCCCTGTGT TGTGGGAGGC TCGGGCTGAG CCATGGGCCA CCTGGGTGCC GCTCCTCTGC 420  
TTTGTGCTCC ATGTCATCTC CTGGCTCCTC ATCTTTAGCA TCCTTCTCGT CTTTGA CTAT 480  
GCTGAGCTCA TGGGCCTCAA ACAGGTATAC TACCATGTGC TGGGGCTGGG CGAGCCTCTG 540  
GCCCTGAAGT CTCCCCGGGC TCTCAGACTC TTCTCCCACC TGCGCCACCC AGTGTGTGTG 600  
GAGTGCTGA CAGTGCTGTG GGTGGTGCTT ACCCTGGGCA CGGACCGTCT CCTCCTTGCT 660  
TTCCTCCTTA CCCTCTACCT GGGCCTGGCT CACGGGCTTG ATCAGCAAGA CCTCCGCTAC 720  
CTCCGGGCCC AGCTACAAAG AAAACTCCAC CTGCTCTCTC GGCCCCAGGA TGGGGAGGCA 780  
GAGTGAGGAG CTCACTCTGG TTACAAGCCC TGTTCCTCCT CTCCCACTGA ATTCTAAATC 840  
CTTAACATCC AGGCCCTGGC TGCTTCATGC CAGAGGCCCA AATCCATGGA CTGAAGGAGA 900  
TGCCCTTCT ACTACTTGAG ACTTTATTCT CTGGGTCCAG CTCCATACCC TAAATTCTGA 960

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GTTTCAGCCA CTGAACTCCA AGGTCCACTT CTCACCAGCA AGGAAGAGTG GGGTATGGAA 1020  
GTCATCTGTC CCTTCACTGT TTAGAGCATG AACTCTCCC CCTCAACAGC CTCCTGAGAA 1080  
GGAAAGGATC TGCCCTGACC ACTCCCCTGG CACTGTTACT TGCCTCTGCG CCTCAGGGGT 1140  
CCCCTTCTGC ACCGCTGGCT TCCACTCCAA GAAGGTGGAC CAGGGTCTGC AAGTTCAACG 1200  
GTCATAGCTG TCCCTCCAGG CCCCAACCTT GCCTCACCAC TCCCGGCCCT AGTCTCTGCA 1260  
CCTCCTTAGG CCCTGCCTCT GGGCTCAGAC CCCAACCTAG TCAAGGGGAT TCTCCTGCTC 1320  
TTAACTCGAT GACTTGGGGC TCCCTGCTCT CCCGAGGAAG ATGCTCTGCA GGAAAATAAA 1380  
AGTCAG 1386

(2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 542 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:  
(A) LIBRARY: LATRTUT02  
(B) CLONE: 1405329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91 :

CCCGGGCCAT GCAGCCTCGG CCCCGCGGGC GCGCGCCGCG CACCCGAGGA GATGAGGCTC 60  
CGCAATGGCA CCTTCCTGAC GCTGCTGCTC TTCTGCCTGT GCGCCTTCCT CTCGCTGTCC 120  
TGGTACGCGG CACTCAGCGG CCAGAAAGGC GACGTTGTGG ACGTTTACCA GCGGGAGTTC 180  
CTGGCGCTGC GCGATCGGTT GCACGCAGCT GAGCAGGAGA GCCTCAAGCG CTCCAAGGAG 240  
CTCAACCTGG TGCTGGACGA GATCAAGAGG GCCGTGTCAG AAAGGCAGGC GCTGCGAGAC 300  
GGAGACGGCA ATCGCACCTG GGGCCGCCTA ACAGAGGACC CCCGATTGAC GCCGTGGAAC 360  
GGCTCACACC GGCACGTGCT GCACCTGCCC ACCGTCTTCC ATCACCTGCC ACACCTGCTG 420  
GCCAAGGAGA GCAGTCTGCA GCGCGCGGTG CGCGTGGGCC AGGGCCGCAC CGGAGTGTCTG 480  
GTGGTGATGG GCATCCCGAG CGTGCGGCGC GAGGTGCACT CGTACCTGAC TGACACTCTG 540  
CA 542

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAINOT12
- (B) CLONE: 1415223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92 :

CGAGCCCGGA GTGCGGACAC CCCCGGGATG CTTGCGCCCC AGAGGACCCG CGCCCCAAGC 60  
CCCCGCGCCG CCCCCAGGCC CACCCGGAGC ATGCTGCCTG CAGCCATGAA GGGCCTCGGC 120  
CTGGCGCTGC TGGCCGTCCT GCTGTGCTCG GCGCCCGCTC ATGGCCTGTG GTGCCAGGAC 180  
TGCACCCTGA CCACCAACTC CAGCCATTGC ACCCAAAGC AGTGCCAGCC GTCCGACACG 240  
GTGTGTGCCA GTGTCCGAAT CACCGATCCC AGCAGCAGCA GGAAGGATCA CTCGGTGAAC 300  
AAGATGTGTG CCTCCTCCTG TGACTTCGTT AAGCGACACT TTTTCTCAGA CTATCTGATG 360  
GGGTTTATTA ACTCTGGGAT CTTAAAGGTC GACGTGGACT GCTGCGAGAA GGATTTGTGC 420  
AATGGGGCGG CAGGGGCAGG GCACAGCCCC TGGGCCCTGG CCGGGGGGCT CCTGCTCAGC 480  
CTGGGGCCTG CCCTCCTCTG GGCTGGGCCC TGATGTCTCC TGCTTCCCAC GGGGCTTCTG 540  
AGCTTGCTCC CCTGAGCCTG TGGCTGCCCT CTCCCCAGCC TGGCGTGGCT GGGGCTGGGG 600  
GCAGCCTTGG GCCAGCTCCG TGGCTGTGGC CTGTGGGTCT GAATTCTTCC CCGACGTGAA 660  
GCCTNCCTGT CTCTCCGGCA GCTCTGAGTC CCAGGCAGCT GGACATTCCA GGGGAACAAG 720  
CCATTNGGCA GGAGGGCTGG GATGAGGTTG GGGGGGACCG GAGGTCCCGG AG 772

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1738 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAINOT12
- (B) CLONE: 1416553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93 :

TGTCCATCCA AAAACCATAA AATCACTGGG TTCCACATCA GCCTCCATGA GGCCAAGCCT 60  
TGTACCTGCA AGCTCTTGGC CTAACCATTC CTCTGTCTC TTCTCTGGCC TGCCTGGGGA 120  
GCCCCGTGAAG GCCGCACGGG TGCCTCCAGC CTGAGACATC AGGGGAGAGC CTGCAGCTGA 180

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GTTCAGCAGA AAGGAGGAAT CCTGGCCCTC AGGAAGAAGA TAGTCACATG TTTTCTTCC 240  
TTGTCCCCAC AGCCCCCAGA ACAACATTCT CCCTGCTGGC AGCCCTTCCA TGTCTCCAAA 300  
CCTGGGTCAG AGTGAAAGGA CCTTTGGGGG TGGGTGGGAG CAAAGGGCCC ACCTGCTGGT 360  
TGGTGAAAGC AGTGGTGCCG GAGTGCTAGG TACCGCACGA GTAGTGGTGC GGGGGCTTGG 420  
GAAGCAGACC AGGGTTGGAC AAAACCCCAT GAGGGCGGGG AGCTGGAAGA AAAGTCTCTT 480  
GGGGACCTCT GGGGCAAGGA GCTGAGAAGT CCTGCAGCAC CAGGTGAGAC TTGCTTACAG 540  
TGGATGCCAC TTCTAGGCCT CTGGACCGCA GATGCCCTCC TCCCTCCTGC ACACCTGGCC 600  
TCCTGGGCCT CCAGGTAAAG AGAGAGAGCC AGCCCAGCCC TGTTTCCCCT CAGTCCTCCT 660  
TTGCTCCTGC TGCTTCTCCC AACAGCCCAC TGTTAGGAGG TAGTAGACCC CAGCCTCAAG 720  
GCTCTGACCT TCTTCATGTG GGCACAGAGG GTCCTGACAC TCTGGCAGGG CCTGAGCTGG 780  
GGCAGGCCTC CCTCAGGGCC AGGGGCGATG GCACCCCGGG GACAGGCAGA CCTCCTTCCT 840  
GCCGTCAGCA CCCCCTTCCT TATCACTGTC TGGTCTCCGA GCTTCGGCTG CAGCCTGAGG 900  
TGTGTCCTGG GCTCCTCAGA GCCTGAAGCA AGCTTTTGGA AGCCTGCAGT CCTCCCAGCT 960  
CCAGTGCAGA AGCCTCTCTC TCCAGCCTTT CCCCAGGCAG GAGTTGGGGT TGGGGGCCTC 1020  
TGTCCTCAT CGCTTACCTT GGAAAGGTGG GAAGCTGGCA ATCTGCACCT TGGGGCCTGG 1080  
GCTCCCCCTC TCTGTGCCAG CGGCTTCCCA GCACCTGGGA GGGGCTGCAG CCCCAGCTGG 1140  
ACTCCAGCCT GTCCCTCTTA GCACTCTAGC TGCCCACTCC AGGGCAGGGA CTCGAAACCC 1200  
CCTCCGTCCT GAGCAGCCAC CTCCAGGGCC CTGTTTGGA CCACTCTCTC AGTCCCCAGG 1260  
TCCTCAGGGC CCCAGAGCGG GAGGGTCTCC TACCTGGAAG TCCCCCTGAG CTCCAGGGCC 1320  
CAGCCCTACC TGCCAGTGCT GGTGTCAGGG CACTCAACAC CGAGTGTGGG GGCCACGCCC 1380  
CTTGCCATGC CCACGGCCTC CTCCTGTAGC CCCTGCCTGC ACCCACGATG CTGCACGGGC 1440  
CCGCCCTGGT GGGGCTCGGC GAGTAATGTG TTTTGTCCCC AGTTAACCAC CATTCTGCGG 1500  
CCTGGTTCTG CAAGGAACCA GGGCTGCCCC ACCGCCCGCC GTCTGCCGCC CTAGGCTTCC 1560  
TGACTCCATT AGTTCCGACA CTTGTGAAAC TCCGAGAAGT GCTGTGGTCT CAGCAATGCA 1620  
CCTGTTTTGT ACATGATTGT GTAATTTAAA GGTATATAAA TACAAATATA TATATATATC 1680  
AGTTGTGATT GTATGACTGT GGATAAAATC CAGAACTGTG TCAACCTGAA AAAAAAAA 1738

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2100 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: KIDNNOT09  
(B) CLONE: 1418517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94 :

GGGAAAGCGG CGAGTAAGAT GGAAGATGAG GAGGTCGCTG AGAGCTGGGA AGAGGCGGCA 60  
GACAGCGGGG AAATAGACAG ACGGTTGGAA AAAAAACTGA AGATCACACA AAAAGAGAGC 120  
AGGAAATCCA AATCTCCTCC CAAAGTGCCC ATTGTGATTC AGGACGATAG CCTTCCCGCG 180  
GGGCCCCCTC CACAGATCCG CATCCTCAAG AGGCCCACCA GCAACGGTGT GGTCAGCAGC 240  
CCCAACTCCA CCAGCAGGCC CACCCTTCCA GTCAAGTCCC TAGCACAGCG AGAGGCCGAG 300  
TACGCCGAGG CCCGGAAGCG GATCCTGGGC AGCGCCAGCC CCGAGGAGGA GCAGGAGAAA 360  
CCCATCCTCG ACAGGCCAAC CAGGATCTCC CAACCCGAAG ACAGCAGGCA GCCCAATAAT 420  
GTGATCAGAC AGCCTTTGGG TCCTGATGGG TCTCAAGGCT TCAAACAGCG CAGATAAATG 480  
CAGGCAAGAA AAGATGCCGC CGTTGCTGCC GTCACCGCCT CCTGGGTCGT CCGCCACGGG 540  
TTGCACTGCC GTGGCAGACA GCTGGACTTG AGCAGAGGGA ACGACCTGAC TTACTTGCAC 600  
TGTGATCCCC CTTGCTCCGC CCACTGTGAC CTTGAACCCC ATGCACTGTG ACCTCCCCCC 660  
TTCTCCCCCT TCCCACTGTG ATTGGCACAT CGACAAGGGC TGTCCCAAGT CAATGGAAAG 720  
GGAAAGGGTG GGGGTTAGGG GAAGGTTGGG GGGACCCAGC AAGGACTCAG AGAGTCAGAC 780  
AGTGCCACTT GGCCACTTGG GGTAAAGCCA GTGCCAGCAA TAACAGTTTA TCATGCTCAT 840  
TAATTTGGGA TTTCAAACA CAAATGAAAA CTCACACCCA CCCACCCCA AGTGCATGTC 900  
TCCATCACTT AAAAAGTAAG TTCCATTTGA AAATATCCTT TCTTTTTTTT TTCTTCTAT 960  
TTTTGTTTGT TTATACAAAT ATCTGATTTG CAAGAAAAAG TGCATGGGAG GGGTTTTAGT 1020  
GGTTTAATGA ATTTTAAATT AAGAAAGGGT AGTTTGGTAG TCTACTTAAA AATGTTTCTG 1080  
GGAAATTCAC TAGAAACATT AACCAATAGG ATTTTGGTGA GCTTAGCTTC TGTATTCTTA 1140  
CTGCCGCCCA GAAAAGGGGC AGGGCTCTGC AGCCGCCAGG ACAGACGAGC ACCCATGCC 1200  
TATACCTCCC TCCCCGAGCT AAGTCCCAGG GCATCTGGGC CTTGCCTGGA GACTGGGCTA 1260  
GCTCTGTAGG CTCGGAGAGC CTGGGGAGGG TGCCAACCCC ACCTCTAGTA TTTTGGGAGA 1320  
TAGGGAAAGT GAACCGACTT CCCCTTCCCA TACCCCTCAG GGTGGTTCCC TACCAGCCAG 1380  
GCTTACTACT TCTAGAAGAA AGCAGAGTGC CAGGGAGTGA GATTGCATCC CTGGGCTTAG 1440  
AAGTGACGGA GAGAAGACTT GTTTAGTATT TTGCCATCAG CACAAGGAAA ACCAGGAGAG 1500  
AGTCTGCCTC CAGGACTCTG AGCCTTCTGC CTCGTATGTT CAGAAGGTGG ATAGGTCTTC 1560



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CCACTCCAGC ATGGCTTGAA CTCTTAGGGG TCTGCAGTGC TCCATCTCCA TTGGTGGCCC 1620  
CAGCTCAGTA ACTATACCTG GTACATTTCC TGTGTGCAAT CAGTACCTTG AAGGCAGAAC 1680  
ATTCTGAATA AAGTTGGAAA AAGAACAGCT TTGCTTTGCA AAGATTGATG ACAGACTGGT 1740  
TCCTCAGAGG CCTAGGCTAC CCGTCACCCC TTTTTCAGAG GCGAGGGCCT GGAATGAAGG 1800  
CAGTTTATCC TCTGTCCCTG GAGCCTGGGG TTTGCTTTGG CTCCTTGAGG TGGAAGAGAC 1860  
TAAGAGGGCA GCTGCCCAGA GCAGCTGTGT GTACCTGGCT CCTCTCAGGC TTCCTGATCC 1920  
CTTCCATTGC ACTGCGCCTT ATCCCTCAGC CAGCCAGACA GCCTCCCTGC TCCTGACCAG 1980  
CAGATACGTT TCGGAGTGGT TGGTGTGGTT TTTGTGATGA GGGCAGCACA TGGTGGCCAA 2040  
GGTGGGCAAA GCTGAGTCTC ACAAGGCTCA AATCCCTTCG GTTGGGNTCC CCTTGTGGGG 2100

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PANCNOT08
- (B) CLONE: 1438165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95 :

GCGGGCGGAG ATGTAGACCC GGTAGTGTTG TGCCTTGTGG TGACAACTGG CGGCAGCGCG 60  
CCGCGGGCCC GAGACTTAGT CTCGGGCCGC CATGGCCAGC GTCCACGAGA GCCTCTACTT 120  
CAATCCCATG ATGACCAATG GGGTTGTGCA CGCCAATGTG TTCGGCATCA AGGACTGGGT 180  
GACGCCGTAC AAGATCGCGG TGCTGGTGCT GCTGAACGAG ATGAGCCGCA CAGGCGAGGG 240  
CGCCGTCAGC CTCATGGAGC GGCGGAGGCT CAACCAGCTG CTCCTGCCCC TGCTGCAGGG 300  
CCCAGATATT AACTGTCAA AACTTTACAA GTTAATTGAA GAGTCTTGTC CACAGCTGGC 360  
AAATTCAGTG CAGATCAGAA TCAAACGAT GGCTGAAGGC GAGTTGAAGG ATATGGAACA 420  
GTTTTTTGAT GACCTTTCAG ATTCTTTCTC TGGAACGAA CCAGAGGTTT ACAAACAAG 480  
TGTAGTAGGT TTGTTTCTGC GTCACATGAT CTTGGCCTAC AGTAAGCTTT CTTTCAGCCA 540  
AGTGTTTAAA CTGTACACTG CCCTTCAGCA GTACTTCCAG AATGGTGAGA AAAAGACAGT 600  
GGAGGATGCT GATATGGAAC TGACCAGTAG AGATGAGGGT GAAAGAAAAA TGGAAGAAAG 660  
AGAACTTGAT GTATCTGTAA GAGAAGAGGA GGTATCTTGC AGTGGGCCTC TGTCCCAAAA 720  
ACAAGCAGAA TTTTTTCTTT CTCAACAGGC TTCTTTGCTA AAGAATGATG AGACTAAGGC 780

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CCTCACTCCA GCTTCCTTGC AGAAGGAATT AAACAATTTG TTGAAATTTA ATCCTGATTT 840  
TGCTGAAGCG CATTATCTCA GCTACTTAAA CAACCTCCGT GTCCAAGATG TTTTCAGTTC 900  
AACACACAGT CTCCTCCATT ATTTTGATCG TCTGATTCTT ACCGGAGCCG AAAGCAAAAG 960  
TAATGGGGAA GAGGGCTATG GCCGGAGCTT GAGATACGCC GCTCTGAATC TTGCCGCCCT 1020  
GCACTGCCGC TTCGGTCACT ATCAACAGGC AGAGCTCGCC CTGCAGGAGG CAATTAGGAT 1080  
TGCCCAGGAG TCCAACGATC ACGTGTGTCT CCAGCACTGT TTGAGCTGGC TTTATGTGCT 1140  
GGGGCAGAAG AGATCCGATA GCTATGTTCT GCTGGAGCAT TCTGTGAAGA AGGCAGTACA 1200  
TTTTGGGTTA CCGAGAGCTT TTGCTGGGAA GACGGCAAAC AAGCTGATGG ATGCCCTAAA 1260  
GGACTCCGAC CTCCTGCACT GGAAACACAG CCTGTCAGAG CTCATCGATA TCAGCATCGC 1320  
ACAGAAAACG GCCATCTGGA GGCTGTATGG CCGCAGCACC ATGGCACTGC AACAGGCCCA 1380  
GATGTTGCTG AGCATGAACA GCCTGGAGGC GGTGAATGCG GCGTGCAGC AGAACAACAC 1440  
AGAGTCCTTT GCTGTGCAC TCTGCCACCT CGCAGAGCTA CACGCGGAGC AGGGCTGTTT 1500  
TGCTGCAGCT TCTGAAGTGT TAAAGCACTT GAAGGAACGA TTTCCGCTA ATAGTCAGCA 1560  
CGCCCAGTTA TGGATGCTAT GTGATCAAAA AATACAGTTT GACAGAGCAA TGAATGATGG 1620  
CAAATATCAT TTGGCTGATT CACTTGTTAC AGGAATCACA GCTCTCAATA GCATAGAGGG 1680  
TGTTTATAGG AAAGCGGTTG TATTACAAGC TCAGAACCAA ATGTCAGAGG CACATAAGCT 1740  
TTTACAAAAA TTGTTGGTTC ATTGTCAGAA ACTGAAGAAC ACAGAAATGG TGATCAGTGT 1800  
CCTACTGTCC GTGGCAGAGC TGTACTGGCG ATCTTCCTCC CCTACCATCG CGCTGCCCAT 1860  
GCTCCTGCAG GCTCTGGCCC TCTCCAAGGA GTACCGGTTA CAGTACTTGG CCTCTGAAAC 1920  
AGTGCTGAAC TTGGCTTTTG CGCAGCTCAT TCTTGAATC CCAGAACAGG CCTTAAGTCT 1980  
TCTCCACATG GCCATCGAGC CCATCTTGGC TGACGGGGCT ATCCTGGACA AAGGTCGTGC 2040  
CATGTTCTTA GTGGCCAAGT GCCAGGTGGC TTCAGCAGCT TCCTACGATC AGCCGAAGAA 2100  
AGCAGAAGCT CTGGAGGCTG CCATCGAGAA CCTCAATGAA GCCAAGAAGT ATTTTGCAAA 2160  
GGTTGACTGC AAAGAGCGCA TCAGGGACGT CGTTTACTTC CAGGCCAGAC TCTACCATAC 2220  
CCTGGGGAAG ACCCAGGAGA GGAACCGGTG TGCGATGCTC TTCCGGCAGC TGCATCAGGA 2280  
GCTGCCCTCT CATGGGGTAC CCTTGATAAA CCATCTCTAG AGAGGACATC CCTGCTGGGC 2340  
TGCTGTGCAG AGTATAAGAT TTTGGACTTG TTCATGTCCC CTCTCTCCCT ATAAATGATG 2400  
TATTTGTGAC ACCCTATCTT GTCAATAAAC AGCATTCTGA TTAAAAAAA AAAAAAAA 2458

(2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2900 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: THYRNOT03  
 (B) CLONE: 1440381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96 :

TGCATGGATG GGATACTGGA TGAATCTTTG CTTGAAACCT GTCCAATTCA GTCACCATTA 60  
 CAAGTTTTTG CAGGAATGGG TGGACTGGCT CTTATTGCTG AAAGACTACC CATGCTATAT 120  
 CCAGAAAGTAA TTCAACAGGT GAGTGCTCCA GTTGTAACAT CTACCACTCA GGAAAAGCCG 180  
 TATGATAGCG ATCAGTTTGA ATGGGTGACC ATTGAACAGT CAGGGGAGTT AGTTTATGAA 240  
 GCACCAGAAA CTGTTGCGGC TGAACCTCCA CCTATCAAGT CAGCAGTACA GACCATGTCT 300  
 CCCATACCTG CCCATTCTTT GGCTGCTTTT GGATTATTTT TTCGTCTTCC GGGCTATGCG 360  
 GAAGTGCTAC TGAAAGAGAG AAAACATGCC CAGTGCCTTC TTCGATTGGT ATTGGGAGTG 420  
 ACAGATGATG GAGAAGGAAG TCATATTCTT CAATCTCCAT CAGCCAATGT GCTTCCAACC 480  
 CTTCCCTTCC ACGTCCTTCG TAGCTTGTTT AGCACTACAC CTTTGACAAC TGATGATGGT 540  
 GTACTTCTAA GGCGGATGGC ATTGGAAATT GGAGCCTTAC ACCTCATTCT TGTCTGTCTC 600  
 TCTGCTTTGA GCCACCATTG CCCACGAGTT CCAAACCTCTA GCGTGAATCA AACTGAGCCA 660  
 CAGGTGTCAA GCTCTCATAA CCCTACATCA ACAGAAGAAC AACAGTTATA TTGGGCCAAA 720  
 GGGACTGGCT TTGGAACAGG CTCTACAGCT TCTGGGTGGG ATGTGGAACA AGCCTTAACT 780  
 AAGCAAAGGC TGGAAGAGGA ACATGTTACC TGCCTTCTGC AGGTTCTTGC CAGTTACATA 840  
 AATCCCGTCA GTAGTGCGGT AAATGGAGAA GCTCAGTCAT CTCATGAGAC TAGAGGGCAG 900  
 AACAGTAATG CCCTTCCTTC TGTACTTCTC GAGCTTCTCA GTCAGTCCTG CCTCATCCCA 960  
 GCCATGTCAT CTTATCTACG AAATGATTCA GTTCTGGACA TGGCAAGACA TGTGCCACTC 1020  
 TATCGGGCAC TGCTGGAATT GCTTCGGGCC ATTGCTTCTT GTGCTGCCAT GGTGCCCCCTA 1080  
 TTGTTGCCCC TTTCTACAGA GAACGGTGAA GAGGAAGAAG AACAGTCAGA ATGTCAAACCT 1140  
 TCTGTTGGTA CATTGTTAGC CAAAATGAAG ACCTGTGTTG ATACCTATAC CAACCGTTTA 1200  
 AGATCTAAAA GGGAAAATGT TAAAACAGGA GTAAAACCAG ATGCGTCTGA TCAAGAACCA 1260  
 GAAGGACTTA CTCTTTTGGT ACCAGACATC CAAAAGACTG CTGAGATAGT TTATGCAGCC 1320  
 ACCACCAGTT TGCGGCAAGC AAATCAGGAA AAAAAGCTGGG TGAATACTCC AAGAAGGCGG 1380  
 CTAATGAACC CCAAACCTTT GTCAGTATTA AAGTCACTTG AAGAAAAATA TGTGGCTGTT 1440  
 ATGAAGAAAT TACAGTTTGA TACGTTTGAA ATGGTTTCTG AAGATGAAGA TGGGAAATTG 1500

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GGATTTAAAG TAAATTACCA CTACATGTCT CAGGTGAAAA ATGCTAATGA TGCGAACAGT 1560  
GCTGCCAGAG CTCGCCGCCT TGCCCAGGAA GCTGTGACGC TTTCAACCTC ACTGCCTCTG 1620  
TCTTCATCCT CTAGTGTGTT TGTACGCTGT GATGAGGAGC GACTTGATAT CATGAAGGTT 1680  
CTAATAACTG GTCCAGCGGA CACCCCTTAT GCAAATGGCT GCTTTGAGTT TGATGTGTAT 1740  
TTTCCTCAAG ATTATCCCAG TTCACCCCTT CTTGTGAATC TAGAGACAAC TGGTGGTCAT 1800  
AGCGTGCGAT TCAATCCAAA CCTTTATAAT GATGGCAAGG TTTGTTTAAG CATCTTAAAC 1860  
ACGTGGCATG GAAGACCAGA AGAGAAGTGG AATCCTCAGA CCTCAAGCTT TTTGCAAGTG 1920  
TTGGTGTCTG TCCAGTCCCT TATATTAGTA GCTGAGCCTT ATTTTAATGA ACCGGGATAT 1980  
GAACGGTCTA GAGGCACTCC CAGTGGCACA CAGAGTTCTC GAGAATATGA TGGAAACATT 2040  
CGACAAGCAA CAGTTAAGTG GGCAATGCTA GAACAAATCA GAAACCCTTC ACCATGTTTT 2100  
AAAGAGGTAA TACACAAACA TTTTACTTG AAAAGAGTTG AGATAATGGC CCAATGTGAG 2160  
GAGTGGATTG CGGATATCCA GCAGTACAGC AGTGATAAGC GGGTAGGCAG GACTATGTCT 2220  
CACCATGCAG CAGCTCTCAA GCGTCACACT GCTCAGCTCC GCGAAGAGTT GCTGAAACTT 2280  
CCCTGCCCTG AAGGCTTGGA TCCTGACACT GACGATGCC CAGAGGTGTG CAGAGCCACA 2340  
ACAGGTGCTG AGGAGACTCT AATGCATGAT CAGGTTAAAC CCAGCAGCAG CAAAGAACTC 2400  
CCCAGTGACT TCCAGTTATG AGCTGCATTG ATGTGGACTT CATAGACACA AAGGCTTCGA 2460  
AGCACAAGCC AAATATGTCA ATATTTGTAT GTAAGAACT AATTATGTAA TAGGTAATGA 2520  
AACTGAACT ATACTATGCC CTTAAGGAGA TCCAGTTTAA TTCAAGGTGA TCTTTTATTT 2580  
ACCTGTACAG GAGTGTAAC TTTTTTGTGC TTTTATTTTT CAATTGTGAG AACCCTGAT 2640  
TGGTATGTTT AACAAATTTG TGTATACAAA GAAATGGATA AATCACTGCT ATATAAGGGA 2700  
AACTACCTTA GGAAAGAATG TTTACTGAAT GTTTATTTTT TTTTATTTTT TTTTACTAT 2760  
AGAGTGAGGG GTTGTTAACA AAGAATATAT ATTGGTCGTT CTTACAATA CTATTTAAAG 2820  
TCAGCAACTT TTTACTGAAT TTGATAGATT TTATGTTTGG GGGTACGAGC TTGTAAAGCT 2880  
CGGGTGCCTN ATGAGTGACC 2900

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

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(A) LIBRARY: LUNGNOT14

(B) CLONE: 1510839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97 :

CCGCTGAGAT GTACGAACTT CCGGTTCTCC GGGCAGCTGC CACTGCTGTA GCTTCTGCCA 60  
CCTGCCACGA CCGGGCCTCT CCCTGGCGTT TGGTCACCTC TGCTTCATTC TCCACCGCGC 120  
CTATGGTCCC TCTTGAGACC AGCGTGGCGG GCCTGGCGGC TCCCGGGTGG TGAGAGAGCG 180  
GTCCGGGAAC GATGAAGGCC TCGCAGTGCT GCTGCTGTCT CAGCCACCTC TTGGCTTCCG 240  
TCCTCCTCCT GCTGTTGCTG CCTGAACTAA GCGGGCCCCCT GGCAGTCCTG CTGCAGGCAG 300  
CCGAGGCCCG GCCAGGTCTT GGGCCTCCTG ACCCTAGACC ACGGACATTA CCGCCGCTGC 360  
CACCGGGCCC TACCCCTGCC CAGCAGCCGG GCCGTGGTCT GGCTGAAGCT GCGGGGCCGC 420  
GGGGCTCCGA GGGAGGCAAT GGCAGCAACC CTGTGGCCGG GCTTGAGACG GACGATCACG 480  
GAGGGAAGGC CGGGGAAGGC TCGGTGGGTG GCGGCCCTTG TGTGAGCCCC AACCTGGCG 540  
ACAAGCCCAT GACCCAGCGG GCCCTGACCG TGTGATGGT GGTGAGCGGC GCGGTGCTGG 600  
TGTA CTTCGT GGT CAGGACG GTCAGGATGA GAAGAAGAAA CCGAAAGACT AGGAGATATG 660  
GAGTTTTGGA CACTAACATA GAAAATATGG AATTGACACC TTTAGAACAG GATGATGAGG 720  
ATGATGACAA CACGTTGTTT GATGCCAATC ATCCTCGAAG AAGAGAATGT GCCTTTTGAT 780  
GAAAGAACTT TATCTTTCTA CAATGAAGAG TGGAATTTCT ATGTTTAAGG AATAAGAAGC 840  
CACTATATCA ATGTTGGGGG GGTATTTAAG TTACATATAT TTTAACAACC TTTAATTTGC 900  
TGTTGCAATA AATACCGTAT CCTTTTATTA TATCTTTATA TGTATAGAAG TACTCTATTA 960  
ATGGGCTCAG AGATGTTGGG GATAAAGTAT ACTGTAATAA TTTATCTGTT TGAAAATTAC 1020  
TATAAAACGG TGTTTTCTGA TCGGTTTTTG TTTCTGCTT ACCATATGAT TGTA AATTGT 1080  
TTTATGTATT AATCAGTTAA TGCTAATTAT TTTTGCTGAT GTCATATGTT AAAGAGCTAT 1140  
AAATTCCAAC AACCAACTGG TGTGTAAAAA TAATTTAAAA TTTCTTTTAC TGAAAGGTAT 1200  
TTCCCATTTT TGTGGGGAAA AGAAGCCAAA TTTATTACTT TGTGTTGGGG TTTTAAAAAT 1260  
ATTAAGAAAT GTCTAAGTTA TTGTTTGCAA AACAATAAAT ATGATTTTAG 1310

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2272 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: SPLNNOT04  
(B) CLONE: 1534876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98 :

CCATGCTCCA GGCATACAGA TGTGGTTTCT CGGCTGCACC GGGCCAGGCT GCGGGTGTGC 60  
AGGCGTCTGC AAAGTTGTGC CATGTATCAG CACAGGCTTT GAGACGTCTG GACCCTGTCC 120  
TTCTCCCCGT GAGGGGTTCT TGTTCTTTCT GACTCAGGTG ACTTTTCAGC CCTTCCAATT 180  
CCCCTCTTTT TCTGCCCTCC CCTCCAACCTC AGCCAACCCA GGTGTGGGCA GTCAGGGAGG 240  
GAGGGAGTGT CCCACCACGT TCTCAGGGCA GCCCTTGACT CCTAAGCCCC TTCCTCCTTC 300  
CATTCTGCAT CCCCTCCCCA TCCAACCTAA ATGCCACAG CTGGGGCTGA GCTGTATTCC 360  
TGTGGAGGGA CCTCTGCCGT GCCTCTCTGA GGTCAGGCTG TGCTGTGTGA TGGGCAGGCT 420  
TTGCCCCAGC CCACCCCTGG CAAGGTGCAC TTGTTTTCTG GTTTGTACAA GGTGTCCTGG 480  
GGGCCCCGTCG CTTCCCTGCC AGTGAGGAGT GACTTCTCCC TCTCTTCCAG TCCTGTAGGG 540  
GAGACAAAAC CAGATTGGGG GGCCCAAGGG GAGCATGGAA AAGGCCGGCT CCCCTGTCTT 600  
TCCTTGCTG TCAGAGTCAG GGTAACACAC ACCAAGAGTG GAGTGCGGCC AGCAAGTTTG 660  
AGACCTGCCC GCCCTCCTCG CAGCTCTGCT CTGTGTCCTC AGGAAGTCAC AGAGTCTACT 720  
GAGGCAAGGA GAGGGTGATT CTTTCCCCAA ATCCCTTCTT CCCTGGTTCC CAAACCAAAG 780  
ACAGCCTGCA GCCCTTTCTG CATGGGGTGC TCTGTTGACA GGCTTCCCAG ATCCCTGAGT 840  
CTCTCTTTCC TTCCTCCTCG ATCTTTAGTT GTCCACGGTC AATTCAGTGC TTCCATTGGG 900  
GGACAGTCCC CTCCGGGATG ACCTGATTCA CCTCCAGCCC AGGGAATGGA ATCTAGAGGA 960  
ATACGTGGGG TGGGTCTGGA CAAGGAGCGG CAGGAATCAC CACCCATCTC CAGCTGTGGA 1020  
GCCCTGTGGA GGGGAAGGGG AAGCTTGGGG TTCAGAGGGA ACTCTTCCAG GAGAGGGGTG 1080  
CCCAGCGGAG GTAAAGATGA TAGAGGGTTG TGGGGGGTCT CTAGTTGAAT GTTTTGGCCC 1140  
ATGACTTTGG AACATGGCTG GCAGCTTCCA GCAGAAGTCA CGCTCCCCAT CCCCAGGGG 1200  
ACATAGGACC TTTTTCCTGC TTCCTGGTCA CTTTCAAAGA ACTATTTGCG CAATCTGTGG 1260  
GTCTGTGGAT TCACGGGGCT TTCTGTGTGG GTGCTGCAGT TGCTTTTGTC TGCAGCAGCA 1320  
GGACACATCT TTCCTCTTAC TCAGCCCTTT ATGGCCCATG GGGAACCTCCG TGGCTCAGGG 1380  
AGAGCTGAAC TCCAGGGGTG TGACCTGGGA CAGGTGGGCC TGAGGTGCCC AGCTCAGGGC 1440  
AGCCAGGTGG CTCATGGGCT GTAGTGAGCC AGCTCCCTGG GGGAAAAGGC TGTGGGCCGT 1500  
TAGGACCATC CTCCAGGACA GGTGACCTCT ATGAGGTCAC CTACGGCTGT GGCCGTGCAG 1560  
GCCTCCTTCC AGCCAGAGT GGCCAGTAG AGCAAGGCAG ACAGTGACCT CCACCCCCGC 1620  
AGCCCTCTTA AAAGGCCAGT ACTCTTGGGG GTGGGGGGAG GGTTTAGAAA GCATTTGCCC 1680

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ATCTGCCTTT CTTTCCCCCA GCCCCACCC GCTTTGAATG TAGAGACCCG TGGGCACTTT 1740  
TCCTTTTGTG GTGGGGGGTG CGGAGGAGGT ACCCCCACCC CTGGCACAGC CGCCTGGAAT 1800  
GCAGGACTGT CACTGCTGTT CGGGTGATGA CCTCGTTGCC AAGCTCCTCC TGTCCCCTTG 1860  
TTCTGGGGGC AGGCGCTGTG CTTCTGTGAG GTGGTTTAGC TTTTGCTTTC GAAGTGGCCA 1920  
GCTGCGGCCA CCAGGTCTCA GCACAAGAGC GCTTCCTTTG CACAGAATGA GCTTCGAGCT 1980  
TTGTTTCAGAC TAAATGAATG TATCTGGGAG GGGTCGGGGG CACGAGTTGA TTCCAAGCAC 2040  
ATGCCTTTGC TGAGTGTGTG TGTGCTGGGA GAGTCAGAGT GGATGTAGAG CGCGGTTTTA 2100  
TTTTTGTACT GACATTGGTA AGAGACTGTA TAGCATCTAT TTATTTAGAT GATTTATCTG 2160  
GTAAATGAGG CAAAAAATT ATTAAAAATA CATTAAAGAT GATTTAAAAA AAAGACCAAA 2220  
AAACCAAGAA ACCCAAAGCC CAAGAATGCG CGTAGCATCC AAAAAAAAAA GG 2272

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1060 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SPLNNOT04
- (B) CLONE: 1559131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99 :

GTCAACTTAG CGAGCGCAAC AGGCTGCCGC TGAGGAGCTG GAGCTGGTGG GGAAGTGGGCC 60  
GCAATGGACA AGCTGAAGAA GGTGCTGAGC GGGCAGGACA CGGAGGACCG GAGCGGCCTG 120  
TCCGAGGTTG TTGAGGCATC TTCATTAAGC TGGAGTACCA GGATAAAAGG CTTCAATTGCG 180  
TGTTTTGCTA TAGGAATTCT CTGCTCACTG CTGGGTACTG TTCTGCTGTG GGTGCCCAGG 240  
AAGGGACTAC ACCTCTTCGC AGTGTTTTAT ACCTTTGGTA ATATCGCATC AATTGGGAGT 300  
ACCATCTTCC TCATGGGACC AGTGAAACAG CTGAAGCGAA TGTTTGAGCC TACTCGTTTG 360  
ATTGCAACTA TCATGGTGCT GTTGTGTTTT GCACTTACCC TGTGTTCTGC CTTTTGGTGG 420  
CATAACAAGG GACTTGCACT TATCTTCTGC ATTTTGCACT CTTTGGCATT GACGTGGTAC 480  
AGCCTTTCCT TCATACCATT TGCAAGGGAT GCTGTGAAGA AGTGTTTTGC CGTGTGTCTT 540  
GCATAATTCA TGGCCAGTTT TATGAAGCTT TGAAGGCAC TATGGACAGA AGCTGGTGGG 600  
CAGTTTTGTA ACTATCTTCG AAACCTCTGT CTTACAGACA TGTGCCTTTT ATCTTGCAGC 660  
AATGTGTTGC TTGTGATTCG AACATTTGAG GGTTACTTTT GGAAGCAACA ATACATTCTC 720

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GAACCTGAAT GTCAGTAGCA CAGGATGAGA AGTGGGTTCT GTATCTTGTG GAGTGGAATC 780  
TTCCTCATGT ACCTGTTTCC TCTCTGGATG TTGTCCCACT GAATTCCCAT GAATACAAAC 840  
CTATTTCAGCA ACAGCACATA AGCCTTGGGT GCAAGTGATT CCCAGGTGGC AAAAGGCAGC 900  
CCCATCAGAG ATCACGGGAG CAACAGTAAG GGACAGAGTT TTGGGGTCCA CTTGTCCCTC 960  
AGCATGGAAG CCATCACCGT GGTCTGTCAT AGAGTGAGTC TGCTTCTACT CTGGCATCTG 1020  
AGAACAAGTG ACTCTGCTTT AGACAAGCCC CTGGAGAGGG 1060

(2) INFORMATION FOR SEQ ID NO: 100:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 543 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:  
(A) LIBRARY: BLADNOT03  
(B) CLONE: 1601473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100 :

GCTCACAGTA GCCCGGCGGC CAGGGCAATC CGACCACATT TCACTCTCAC CGCTGTAGGA 60  
ATCCAGATGC AGGCCAAGTA CAGCAGCACA AGGGACATGC TGGATGATGA TGGGGACACC 120  
ACCATGAGCC TGCATTCTCA AGCCTCTGCC ACAACTCGGC ATCCAGAGCC CCGGCGCACA 180  
GAGCACAGGG CTCCCTCTTC AACGTGGCGA CCAGTGGCCC TGACCCTGCT GACTTTGTGC 240  
TTGGTGCTGC TGATAGGGCT GGCAGCCCTG GGGCTTTTGT GTAAGTCTGC GCTCTGACCT 300  
GGGGGAGGAT CCTGGTTCCA AGTTTTTCAG TACTACCAGC TCTCCAATAC TGGTCAAGAC 360  
ACCATTTCTC AAATGGAAGA AAGATTAGGA AATACGTCCC AAGAGTTGCA ATCTCTTCAA 420  
GTCCAGAATA TAAAGCTTGC AGGAAGTCTG CAGCATGTGG CTGAAAACT CTGTCGTGAG 480  
CTGTATAACA AAGCTGGAGC ACACAGGTGC AGCCCTTGTA CAGAACAATG GAAATGGCAT 540  
GGA 543

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear



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(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: BRAITUT12  
(B) CLONE: 1615809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101 :

AGCTGGCTCA CCTTCCAGAT TCACCTGCAG GAGCTGCTGC AGTACAAGAG GCAGAATCCA 60  
GCTCAGTTCT GCGTTCGAGT CTGCTCTGGC TGTGCTGTGT TGGCTGTGTT GGGACACTAT 120  
GTTCCAGGGA TTATGATTTT CTACATTGTC TTGTTGAGTA TCCTGCTGTG GCCCTGGTG 180  
GTTTATCATG AGCTGATCCA GAGGATGTAC ACTCGCCTGG AGCCCCTGCT CATGCAGCTG 240  
GACTACAGCA TGAAGGCAGA AGCCAATGCC CTGCATCACA AACACGACAA GAGGAAGCGT 300  
CAGGGGAAGA ATGCACCCCC AGGAGGTGAT GAGCCACTGG CAGAGACAGA GAGTGAAAGC 360  
GAGGCAGAGC TGGCTGGCTT CTCCCCAGTG GTGGATGTGA AGAAAACAGC ATTGGCCTTG 420  
GCCATTACAG ACTCAGAGCT GTCAGATGAG GAGGCTTCTA TCTTGAGAG TGGTGGCTTC 480  
TCCGTATCCC GGGCCACAAC TCCGCAGCTG ACTGATGTCT CCGAGGATTT GGACCAGCAG 540  
AGCCTGCCAA GTGAACCAGA GGAGACCCTA AGCCGGGACC TAGGGGAGGG AGAGGAGGGA 600  
GAGCTGGCCC CTCCCGAAGA CCTACTAGGC CGTCCTCAAG CTCTGTCAAG GCAAGCCCTG 660  
GACTCGGAGG AAGAGGAAGA GGATGTGGCA GCTAAGGAAA CCTTGTTGCG GCTCTCATCC 720  
CCCCCTCCACT TTGTGAACAC GCACTTCAAT GGGGCAGGGT CCCCCAAGA TGGAGTGAAA 780  
TGCTCCCCCTG GAGGACCAGT GGAGACACTG AGCCCCGAGA CAGTGAGTGG TGGCCTCACT 840  
GCTCTGCCCG GCACCCTGTC ACCTCCACTT TGCCTTGTG GAAGTGACCC AGCCCCCTCC 900  
CCTTCCATTC TCCCACCTGT TCCCCAGGAC TCACCCAGC CCCTGCCTGC CCCTGAGGAA 960  
GAAGAGGCAC TCACCACTGA GGACTTTGAG TTGCTGGATC AGGGGGAGCT GGAGCAGCTG 1020  
AATGCAGAGC TGGGCTTGGA GCCAGAGACA CCGCCAAAAC CCCCTGATGC TCCACCCCTG 1080  
GGGCCCCGACA TCCATTCTCT GGTACAGTCA GACCAAGAAG CTCAGGCCGT GGCAGAGCCA 1140  
TGAGCCAGCC GTTGAGGAAG GAGCTGCAGG CACAGTAGGG CTTCTTGGCT AGGAGTGTG 1200  
CTGTTTCCTC CTTTGCCTAC CACTCTGGGG TGGGGCAGTG TGTGGGGAAG CTGGCTGTG 1260  
GATGGTAGCT ATTCCACCCT CTGCCTGCCT GCCTGCCTGC TGTCCCTGGG ATGGTGCAGT 1320  
ACCTGTGCCT AGGATTGGTT TTAAATTTGT AAATAATTTT CCATTGCGT TAGTGGATGT 1380  
GAACAGGGCT AGGGAAGTCC TTCCCACAGC CTGCGCTTGC CTCCCTGCCT CATCTCTATT 1440  
CTCATCCAC TATGCCCCAA GCCCTGGTGG TCTGGCCCTT TCTTTTCTCT CCTATCTCA 1500  
GGGACCTGTG CTGCTCTGCC CTCATGTCCC ACTTGTTGTT TTAGTTGAGG CACTTTATAA 1560  
TTTTTCTCTT GTCTTGTGTT CCTTTCTGCT TTATTTCCCT GCTGTGTCCT GTCCTTAGCA 1620  
GCTCAACCCC ATCCTTTGCC AGCTCCTCCT ATCCCGTGGG CACTGGCCAA GCTTTAGGGA 1680

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GGCTCCTGGT CTGGGAAGTA AAGAGTAAAC CTGGGGCAGT GGGTCAGGCC AGTAGTTACA 1740  
CTCTTAGGTC ACTGTAGTCT GTGTAACTT CACTGCATCC TTGCCCCATT CAGCCCGGCC 1800  
TTTCATGATG CAGGAGAGCA GGGATCCCGC AGTACATGGC GCCAGCACTG GAGTTGGTGA 1860  
GCATGTGCTC TCTCTTGAGA TTAGGAGCTT CCTTACTGCT CCTCTGGGTG ATCCAAGTGT 1920  
AGTGGGACCC CCTACTAGGG TCAGGAAGTG GACACTAACA TCTGTGCAGG TGTTGACTTG 1980  
AAAAATAAAG TGTTGATTGG CTAGAACTGC TGCCTCCCTG ACTGTGAGCT GCCTTCCACA 2040  
CCCTGCACTG CACTGTGTTT TCTCCTCACC CTTAACCTGC TTCACTCCAG TCTGTTCTGG 2100  
CTGTTTATTA CCTTGTTGCA AAACAGGGCC GAAGCAAGGA TTACCTTGAC AACCTAGCT 2160  
TCTCCTTAGC CATCTTCCTT GACAGTGTGA TCTGTTTAGT GAGATTTAGC ATGTGTGAAT 2220  
AAAGTATATG CAGGAGGAAA TTGCTTTGTC TTCCAATCG GTAGAAATTC GAGACCTAGC 2280  
C 2281

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 992 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT19
- (B) CLONE: 1634813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102 :

GACAGCTTGG CCTACAGCCC GGCGGGCATC AGCTCCCTTG ACCCAGTGGA TATCGGTGGC 60  
CCCGTTATTC GTCCAGGTGC CCAGGGAGGA GGACCCGCCT GCAGCATGAA CCTGTGGCTC 120  
CTGGCCTGCC TGGTGGCCGG CTTCCTGGGA GCCTGGGCCC CCGCTGTCCA CGCCCAAGGT 180  
GTCTTTGAGG ACTGCTGCCT GGCCTACCAC TACCCCAT TG GGTGGGCTGT GCTCCGGCGC 240  
GCCTGGACTT ACCGGATCCA GGAGGTGAGC GGGAGCTGCA ATCTGCCTGC TGCGATATTC 300  
TACCTCCCCA AGAGACACAG GAAGGTGTGT GGGGAACCCCA AAAGCAGGGA GGTGCAGAGA 360  
GCCATGAAGC TCCTGGATGC TCGAAATAAG GTTTTGTCAA AGCTCCGCCA CAACACGCAG 420  
ACCTTCCAAG CAGGCCCTCA TGCTGTAAAG AAGTTGAGTT CTGGAACTC CAAGTTATCA 480  
TCATCCAAGT TTAGCAATCC CATCAGCAGC AGCAAGAGGA ATGTCTCCCT CCTGATATCA 540  
GCTAATTCAG GACTGTGAGC CGGCTCATTT CTGGGCTCCA TCGGCACAGG AGGGGCCGGA 600  
TCTTTCTCCG ATAAAACCGT CGCCCTACAG ACCCAGCTGT CCCACGCCT CTGTCTTTTG 660

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GGTCAAGTCT TAATCCCTGC ACCTGAGTTG GTCCTCCCTC TGCACCCCCA CCACCTCCTG 720  
CCCGTCTGGC AACTGGAAAG AGGGAGTTGG CCTGATTTTA AGCCTTTTGC CGCTCCGGGG 780  
ACCAGCAGCA ATCCTGGGCA GCCAGTGGCT CTTGTAGAGA AGACTTAGGA TACCTCTCTC 840  
ACTTTCTGTT TCTTGCCGTC CACCCCGGGC CATGCCAGTG TGTCCCTCTG GGTCCCTCCA 900  
AAACTCTGGT CAGTTCAAGG ATGCCCCTCC CAGGCTATGC TTTTCTATAA CTTTTAAATA 960  
AACCTTGGGG GTTGATGGAG TCAAAAAAA AA 992

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UTRSNOT06
- (B) CLONE: 1638407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103 :

TCGCCCAGGA GTCATCGGAC GCCAGAATCT GTGTCTCCAG AACGCTATAG CTATGGCACC 60  
TCCAGCTCTT CAAAGAGGAC AGAGGGTAGC TGCCGTCGCC GTCGGCAGTC AAGCAGTTCT 120  
GCAAATTCTC AGCAGGGTCA GTGGGAGACA GGCTCCCCC CAACCAAGCG GCAGCGGCGG 180  
AGTCGGGGCC GGCCAGTGG TGGTGCCAGA CGGCGGCGGA GAGGGGCCCC AGCCGCACCC 240  
CAGCAGCAGT CAGAGCCCGC CAGACCTTCC TCTGAAGGCA GGTGACACTG TGATGGGGAA 300  
ACAGGCTCAG AGAGACATCC GGCTCCGGGT TCGAGCAGAG TACTGCGAGC ATGGGCCAGC 360  
CTTGAGCAG GGCCTGGCAT CCCGGCGGCC CCAGGCGCTG GCGCGGCAGC TGGACGTGTT 420  
TGGGCAGGCC ACCGCAAGTC TGCGCTCAAG GGACCTGGGC TCTGTGGTTT GTGACATCAA 480  
GTTCTCAGAG CTCTCCTATC TGGACGCCTT CTGGGGCGAC TACCTGAGTG GCGCCCTGCT 540  
GCAGGCCCTG CGGGGCGTGT TCCTGACTGA GGCCCTGCGA GAGGCTGTGG GCCGGGAGGC 600  
TGTTGCGCTG CTGGTCAGTG TGGATGAGGC TGAATATGAG GCTGGCCGGC GCCGCCTGTT 660  
GCTGATGGCG GAGGAAGGGG GGCGGCGCCC GACAGAGGCC TCCTGATCCA GGAAGTGGCAG 720  
GATTGATCCC ACCTCCAAGT CTCCGGGCCA CCTTCTCCTG GGAGGACGAC CATCTCTACC 780  
CCTAGAGGAC TGTAATCTTA GCATCTTTGA GGACTGCGAC AGGACCGGGA CAGCAGGCCC 840  
CTTGACAGCC CCTCCACAG GATGTGGGCT CTGAGGCCTA AACCATTTC AGCTGAGTTT 900  
CCTTCCAGC CTCCTCCTAC CCCAGGTGT GCGCCCTTAG CCTCCGAGG CGGGGGCTGG 960

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GCCTGTATCT CAGAAGGGAG GGGCACAGCT ACACACTCAC CAAAGGCCCC CCTGCACATT 1020  
GTATCTCTGA TCTTGGGCTG TCTGCACTGT CACAGGTGCA CACTCTCGCT CATGCTCACA 1080  
CTGCCCCTGC TGAGATCTTC CCTGGGCCTC TGCCCTGGCC TGCTTCCCAG CACACACTTC 1140  
TTTGGCCTAA GGGCTTCTCT CTCAGGACCT CTAATTTGAC CACAACCAAC CTGGGCTTCA 1200  
GCCACATCAG TGGGCACTGG AGCTGGGGTG CACATGGGGC CTGCTCACCT TGCCCACACA 1260  
TCTCCAGCCA GCCAGGGCCC TGCCCAGCTT CAATTTACAG ACCTGACTCT CCTCACCTTC 1320  
CCCCCTGCTG TCCAGAGCTG AACATAGACT TGCATTGGA TGTCACCTGG AGTGTCACAT 1380  
GGGAGTGTTA TGGCAGCATC ATACCAAGGC CTACTGTTGC ACATGGGGCC AAAACAGTA 1440  
AACAGCCACC TTCTTGAAA GGAATGCAA AGGCTTTGGG GGTGATGGAA AAGACCTTTT 1500  
ACAAATGATA CCAATTAAAC TGCCCTGGAA AGGGCATAGG TGGGAAAAAA AAAA 1554

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSTUT08
- (B) CLONE: 1653112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104 :

GTCGCCGGGC TTGCGATGAA CTTCCGGCTG TCAAGCTCCC GGCCGGGCTG ACTCAAGCGG 60  
AGGCGCGCGG AACAGTCGCC GAGGCGATTC CCGCCCAGGC TCCTGTAACC GCCAGGCAGC 120  
GGCCCCGCCA TGTCCCAGCC CCGGACCCCA GAGCAGGCAC TGGATACACC GGGGGACTGC 180  
CCCCCAGGCA GGAGAGACGA GGACGCTGGG GAGGGGATCC AGTGCTCCCA ACGCATGCTC 240  
AGCTTCAGTG ACGCCCTGCT GTCCATCATC GCCACCGTCA TGATCCTGCC TGTGACCCAC 300  
ACGGAGATCT CCCCAGAACA GCAGTTCGAC AGAAGTGTAC AGAGGCTTCT GGCAACACGG 360  
ATTGCCGTCT ACCTGATGAC CTTTCTCATC GTGACAGTGG CCTGGGCAGC ACACACAAGG 420  
TTGTTCCAAG TTGTTGGGAA AACAGACGAC ACACTTGCCC TGCTCAACCT GGCCTGCATG 480  
ATGACCATCA CCTTCCTGCC TTACACGTTT TCGTTAATGG TGACCTTCCC TGATGTGCCT 540  
CTGGGCATCT TCTTGTTCTG TGTGTGTGTG ATCGCCATCG GGGTCGTGCA GGCCTGATT 600  
GTGGGGTACG CATTCCACTT CCCGCACCTG CTGAGCCCGC AGATCCAGCG CTCTGCCCAC 660  
AGGGCTCTGT ACCGACGACA CGTCCTGGGC ATCGTCCTCC AAGGCCCGGC CCTGTGCTTT 720

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GCAGCGGCCA TCTTCTCTCT CTTCTTTGTC CCCTTGCTTT ACCTGCTGAT GGTGACTGTC 780  
ATCCTCCTCC CCTATGTCAG CAAGGTCACC GGCTGGTGCA GAGACAGGCT CCTGGGCCAC 840  
AGGGAGCCCT CGGCTCACCC AGTGGAAGTC TTCTCGTTTG ACCTCCACGA GCCACTCAGC 900  
AAGGAGCGCG TGGGAAGCCTT CAGCGACGGA GTCTACGCCA TCGTGGCCAC GCTTCTCATC 960  
CTGGACATCT GCGAAGACAA CGTCCCGGAC CCCAAGGATG TGAAGGAGAG GTTCAGCGGC 1020  
AGCCTCGTGG CCGCCCTGAG TCGCACC GCGCGCTTCC TGGCGTACTT CGGCTCCTTC 1080  
GCCACAGTGG GACTGCTGTG GTTCGCCCAC CACTCACTCT TCCTGCATGT GCGCAAGGCC 1140  
ACGCGGGCCA TGGGGCTGCT GAACACGCTC TCGCTGGCCT TCGTGGGTGG CCTCCCACTA 1200  
GCCTACCAGC AGACCTCGGC CTTGCGCCGG CAGCCCCGCG ATGAGCTGGA GCGCGTGCCT 1260  
GTCAGCTGCA CCATCATCTT CCTGGCCAGC ATCTTCCAGC TGGCCATGTG GACCACGGCG 1320  
CTGCTGCACC AGGCGGAGAC GCTGCAGCCC TCGGTGTGGT TTGGCGGCCG GGAGCATGTG 1380  
CTCATGTTCG CCAAGCTGGC GCTGTACCCC TGTGCCAGCC TGCTGGCCTT CGCCTCCACC 1440  
TGCCTGCTGA GCAGGTTTCTG TGTGGGCATC TTCCACCTCA TGCAGATCGC CGTGCCCTGC 1500  
GCCTTCCTGT TGCTGCGCCT GCTCGTGGGC CTGGCCCTGG CCACCCTGCG GGTCCTGCGG 1560  
GGCCTCGCCC GGCCCGAACA CCCCCGCCA GCCCCACGG GCCAGGACGA CCCACAGTCC 1620  
CAGCTCCTCC CTGCCCCCTG CTAGCAGCCA CAGAGCCCAC TCCCAGCCGT CCTCACCAGA 1680  
GATGGACCAG GGAGGACAGG ATGCTGGGCA GGGGAAGCCA AGTCACGGGC AGGCCGCAGT 1740  
GGTTCTTGCG TGGCCTGGTT TTATTTTCAT TGTGAAATAT CATGCTCTTA TTTTCAGTCTT 1800  
CA 1802

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT09
- (B) CLONE: 1664634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105 :

GTACCTCGGC TTATTTTATA AACAGGTACT GAAGGAAGCA GAGGCATGTG GAGGACTTCC 60  
CCACCTCGTG CAGCTATTTG GGCCGTGGCA TCTGAAATTT CTTATTTTCTAG AGTCACCCCT 120  
TTGATGACCT TGGCAGTGAA CTGCAGTCAT CTGTTTAGGC CTTTCCATGG CCCACGTCAA 180

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TGCCGGTATT TCTGTTTGTT GCACATTTGA TTTCTTGTT GTTGGCATTT AGAAGGCCCT 240  
CGAGCCGCAC TGAGGGACTG AGCCTGGTGT ATATGGCAGC AAGACTGGAT GGTGGCTTTG 300  
CAGCAGTCTC CAGAGCATTC CATGAGATCC GGGCTCGAAA TCCAGCATTT CAGCCACAAA 360  
CTTTGATGGA CTTTGGCTCA GGTACTGGTT CTGTCACCTG GGCTGCTCAC AGTATTTGGG 420  
GCCAGAGCCT ACGTGAATAT ATGTGTGTGG ACAGATCAGC TGCCATGTTG GTTTTGGCAG 480  
AAAAACTACT GACAGGTGGT TCAGAATCTG GGGAGCCTTA TATTCCAGGT GTCTTTTCA 540  
GACAGTTTCT ACCTGTATCA CCCAAGGTGC AGTTTGATGT AGTAGTGTCA GCTTTTTCCT 600  
TAAGTGACCA GCTACTGACA TTTATACTTT CGTGTAATTC AAGTCTTCTG CATATTTTCC 660  
CCTTTTGTGA ACAGGTACTG GTGGAGAATG GAACAAAAGC TGGGCACAGC CTTCTCATGG 720  
ATGCCAGGGA TCTGGTCCTT AAGGGAAAAG AGAAGTCACC TTTGGACCCT CGACCTGGTT 780  
TTGTCTTGC CCCGTGTCCC CATGAACTCC CTTGTCCCCA GTTGACCAAC CTGGCCTGTA 840  
GCTTCTCACA GGCGTACCAT CCCATCCCCCT TCAGCTGGAA CAAGAAACCA AAGGAAGAAA 900  
AGTTCTCTAT GGTGATCCTT GCTCGGGGGT CTCCAGAGGA GGCTCATCGC TGGCCCCGTA 960  
TCACTCAGCC TGTCTTAAA CGGCCTCGCC ATGTGCATTG TCACTTGTGC TGTCCAGATG 1020  
GGCACATGCA GCATGCTGTG CTCACAGCCC GCCGGCACGG CAGGTATGGG GGGTGTGACC 1080  
AAAATCAGTG GGATGTGGCA GGAAGCTGCA GCCCACGCCA GCATCTGTTT CCACAGGGAT 1140  
TTGTATCGTT GTGCCC GTGT CAGCTCCTGG GGAGATCTTT TACCTGTGCT TACTCCGTCT 1200  
GCGTTTCCTC CATCTACGGC TCAGGATCCC TCTGAGAGTT GATGAGGATG TGTAACAAGT 1260  
ATTTTCTTCT ATCGTGCCTG CCAGGGCTGA AGCTGCCTGG TATCCAGGAG GGAATGCTG 1320  
GTATCCCCAT ATGTCTGTGT TTGTTTGAGA TTTTAAATAA TAAATAATAA ATTTTGAAG 1380  
AATGGAAAAA AAAAA 1395

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1635 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSTUT10
- (B) CLONE: 1690990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106 :

CCCTCTTCCT TTTGCGCACG GAAGAACAAA TCACAACAAT CACACACCAG GACTGAATCC 60

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ATCAGCAGAT ACTGCCCTGT GGGAAAGGGCA GAGGAAAGAG AAGACAGACG GACTGACAGA 120  
CACCACAGAG GAACAGGGGA GTTAGCCTGG GACCAATGGA GGAGAAGTAC GAACCCTGGG 180  
AAAAAGACGT GTCAGATGAG AAAGTTCCGG AGAGTCCGAT GTCTCATCGC AGGTGTTACA 240  
TCATCAGGGT TTGCCATTGG AATACTGAGT GGAGATGGGA AAGAGAAAAG TTAAGGGCTG 300  
AAATGGGAGG GGAATGGGAA GAAAAAATGA GAGACAAGAG GGAAATAAGA AAAAACAAAG 360  
AGAGCACAAA GACCAGTTTA GGAGAAAGGA CCAATGGGGA CAGTGGCAGA GTGGCGAGGT 420  
AGGTGAAGGA CTGAGGCACA GCGTCCTGTT GTGGAGGGAG GAAAGGCAAG CGTTCCGAGG 480  
TGGTGAAAAG GAAGGCCTGC TAGGCACGGT GGGGATGAAC GAGGATGCCA TGAGTCACAC 540  
AAAAGACAGT GCTGGTGAGG CCCAGCCACA GGAGCCTCAG ATAACTTGGT AAAGGCATGT 600  
CTCCCATTTG GGAAGTATG TTCCTAAGAT CCGCACTGAC GCTGCTCAGC CGGTCCATCA 660  
CACAGCAAAG GCGTGAGGAA GGGTCACTGC CCAGCTGGAC TCCAGGGTGG TCCACGCATG 720  
ACAGTCACAC CGAACCTTCA TGAGGATGTG AACTGTTGGC TCCAATTTAC CATTCCCAGC 780  
AATTCCACTC AGATATTTGT ATACTAATGT TCACAGCAGC GTGAACTCCA CAGCAGGTGG 840  
AGTAATGTTT CATTGTGTGC ATATGCCACA TTTTGTTTAT CCATTCATCT GTTGATGCAC 900  
ATTTTCGGTTG TTCCACCTT TGGGCTATTA TTAATAATGC TGCTGTGAAC ATTCCCAAGA 960  
GAAATAGGAA GACGGCTTTG CTAAGAACTA AAAAAGGGAT GGACAACAAG GGCATATACC 1020  
CAGGGGCAGT GTTCTATCAT GACAGCTTTA CTGAGAGCAG AGTAGTTCTG CTCAGAATCA 1080  
GAACACTTGT TCCCTATAGC CCCCCTGATT GCCCCACAAC CACCACCGCA TACTCCCCTT 1140  
TTCCCAACCA TGGGCAGCAG ATTGAGCTAT TAACAGAAGT GTCCTTTTCGC TGGATTTCTC 1200  
AACCCTTTCC TCATCGTCCA CATAGAGAAA CAGTAACAGA TTGCTACTCA CCCAACACCC 1260  
AGGTCAAGTC CAATGCAGGT AGGAATAACA GCAAATCCTT CAATTTCTTG ATTCTGCTCT 1320  
TAAAAATCTT AACAGAGGCT TCCAGGTTCT GAAAAATATT TCTGCATAAA CGTGTGACAC 1380  
TCCATCACGA AACTCCCTTT GGTTATCTGC TTAAACTTAT CGCAAATGTC TGGAACGCTG 1440  
GTGGCTTCCA AAATCAACTC CTGGTGCTGC TTAATTAAGG TCAGGGCCAC CCGGAAGATA 1500  
ATCTTCGAGC CTTCTGTTAAA CAAACAGTCC CAGATCCGAA GCACTGTCTC CACGGGCAAG 1560  
ATGTCCACAA ACAGGCAGAT GAACCAGCGG GACACCAGCA GCGTCCACAG CACACCGAGA 1620  
CGCTCCATCA GGGGG 1635

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1485 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: DUODNOT02  
(B) CLONE: 1704050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107 :

TTTTTGGTCC CGNCNAAAGN CCNAAAACCC GGNACCCGGG AAGCCNCCCC AANNCNAAAN 60  
TTCCCAGTTN GAANCCCGAA GGNAAAACCC CGGAAAAGNA NNCNGCCCN AAANTTCNCG 120  
GGCNAAAACC CGGCCNTTTT TTCCCCCCCC GCGGCCCGTT TTGGGCCCCN GANTTTCCAT 180  
TTAAANTNCC NAGNCTTGGG CAACCTAACC AGGNTTTTCC CCAANCTGG AAAAAGCCGG 240  
GCCAAGTTGA GCCGCACCCG CCCCAGAAGT TCAAGGGCCC CCGGCCTCCT GCGCTCCTGC 300  
CGCCGGGACC CTCGACCTCC TCAGAGCAGC CGGCTGCCGC CCCGGAAGA TGGCGAGGAG 360  
GAGCCGCCAC CGCCTCCTCC TGCTGCTGCT GCGCTACCTG GTGGTCGCCC TGGGCTATCA 420  
TAAGGCCTAT GGGTTTTCTG CCCCAAAAGA CCAACAAGTA GTCACAGCAG TAGAGTACCA 480  
AGAGGCTATT TTAGCCTGCA AAACCCCAAA GAAGACTGTT TCCTCCAGAT TAGAGTGGA 540  
GAAACTGGGT CGGAGTGTCT CCTTTGTCTA CTATCAACAG ACTCTTCAAG GTGATTTTAA 600  
AAATCGAGCT GAGATGATAG ATTTCAATAT CCGGATCAAA AATGTGACAA GAAGTGATGC 660  
GGGGAAATAT CGTTGTGAAG TTAGTGCCCC ATCTGAGCAA GGCCAAAACC TGGAAGAGGA 720  
TACAGTCACT CTGGAAGTAT TAGTGGCTCC AGCAGTTCCA TCATGTGAAG TACCCTCTTC 780  
TGCTCTGAGT GGAAGTGTGG TAGAGCTACG ATGTCAAGAC AAAGAAGGGA ATCCAGCTCC 840  
TGAATACACA TGTTTAAAG ATGGCATCCG TTTGCTAGAA AATCCCAGAC TTGGCTCCCA 900  
AAGCACCAAC AGCTCATACA CAATGAATAC AAAAAGTGA ACTCTGCAAT TTAATACTGT 960  
TTCCAAACTG GACACTGGAG AATATTCCTG TGAAGCCCGC AATTCTGTTG GATATCGCAG 1020  
GTGTCCTGGG AAACGAATGC AAGTAGATGA TCTCAACATA AGTGGCATCA TAGCAGCCGT 1080  
AGTAGTTGTG GCCTTAGTGA TTTCCGTTTG TGGCCTTGGT GTATGCTATG CTCAGAGGAA 1140  
AGGCTACTTT TCAAAGAAA CCTCCTTCCA GAAGAGTAAT TCTTCATCTA AAGCCACGAC 1200  
AATGAGTGAA AATGATTTCA AGCACACAAA ATCCTTTATA ATTTAAAGAC TCCACTTTAG 1260  
AGATACACCA AAGCCACCGT TGTTACACAA GTTATTAAAC TATTATAAAA CTCTGCTTTG 1320  
TCCGACATTT GCAAAGAGGT ACACGAGGAA ATGGAATTGG TATTTCAATTT TAATTTTCAT 1380  
GACTACTAAC TCACCTGAAC TTGCTATTTT AAACAAATAG TTCTGTCGAC ACCTAAAATA 1440  
TAATCTGGCT TCTTGTGTCT GGAATAAGTT AAAAGAATTA AAATA 1485



(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 810 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: PROSNOT16  
 (B) CLONE: 1711840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108 :

CGAGTGAGCG CGCGGCGGCC CCTGGTCCGC CCGGCCGCGG CCGATCTAGG GGCTGGGGGC 60  
 TGGAGGCGGG GGTGGGGGTC TGAGCTGCGT CCTGGGCTCG AGGCGTCCCC CGGGGAGTCG 120  
 CCTCTTAGCG GTGCGTCCGG GCTAGCGGCG AGGGGCCGCC CCAAGTCTTC CCACCGCCGC 180  
 CACCTTAGCA GCCCGACTTG GGGCCTGGAA AGTGGAGCAC GCGGAGGTGG GAGGGCCCTG 240  
 CACGCGGCCC CCGGTGGGGA AGGGGACGGG CCAGGGATTC AGACTCGGGC TCTCCCCTCA 300  
 GGATGCAGCA CCGAGGCTTC CTCCTCCTCA CCCTCCTCGC CCTGCTGGCG CTCACCTCCG 360  
 CGGTCGCCAA AAAGCAAGAT AAGGTGAAGA AGGGCGGCCC GGGGAGCGAG TGCGCTGAGT 420  
 GGGCCTGGGG GCCCTGCACC CCCAGCAGCA AAGGATTGCG GGCAGTGGGT TTTCCGCGAG 480  
 GGCCACCTTG GGGGGGCCCA AGAACCCAAC CGGCAGTCCT GGTGAAAGG GTTGCCCCTG 540  
 GAAAGTTGGA AAGAAAGGAG TTTTGGGCAC CCGGACTTTG GAAAGTTGGC CAAATTTTTT 600  
 GGAAGAAAAC TTGGCGGGTC TGCCGGTCCG TTAAATGGGG GAGGGGACAA AAGAATTGAA 660  
 AGCCGAAAAA ATGCTTTCTC CGCCGCCAAG AGAGGTCGAA CCCGCGTCTG GCAAGAAGAG 720  
 AAAAGGGCGC GCCCACACTG TTAACAACAA TATGGCGCCT GAACAGTTGG TGGCACCACA 780  
 GGGGGAGGGA GACACATACT TGCGCGCGGT 810

(2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1064 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109 :

TTCTTGGGGC TCCGGGGCGC GGAGAAGCTG CATCCCAGAG GAGCGCGTCC AGGAGCGGAC 60

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CCGGGAGTGT TTCAAGAGCC AGTGACAAGG ACCAGGGGCC CAAGTCCCAC CAGCCATGCA 120  
GACCTGCCCC CTGGCATTCC CTGGCCACGT TTCCCAGGCC CTTGGGACCC TCCTGTTTTT 180  
GGCTGCCTCC TTGAGTGCTC AGAATGAAGG CTGGGACAGC CCCATCTGCA CAGAGGGGGT 240  
AGTCTCTGTG TCTTGGGGCG AGAACACCGT CATGTCCTGC AACATCTCCA ACGCCTTCTC 300  
CCATGTCAAC ATCAAGCTGC GTGCCCACGG GCAGGAGAGC GCCATCTTCA ATGAGGTGGC 360  
TCCAGGCTAC TTCTCCCGGG ACGGCTGGCA GCTCCAGGTT CAGGGAGGCG TGGCACAGCT 420  
GGTGATCAAA GGCGCCCGGG ACTCCCATGC TGGGCTGTAC ATGTGGCACC TCGTGGGACA 480  
CCAGAGAAAT AACAGACAAG TCACGCTGGA GGTTTCAGGT GCAGAACCCC AGTCCGCCCC 540  
CGACACTGGG TTCTGGCCTG TGCCAGCGGT GGTCAC TGCTTCATCC TCTTGGTCGC 600  
TCTGGTCATG TTCGCCTGGT ACAGGTGCCG CTGTTCCCAG CAACGCCGGG AGAAGAAGTT 660  
CTTCCTCCTA GAACCCCAAG TGAAGGTCGC AGCCCTCAGA GCGGGAGCCC AGCAGGGCCT 720  
GAGCAGAGCC TCCGCTGAAC TGTGGACCCC AGACTCCGAG CCCACCCCAA GGCCGCTGGC 780  
ACTGGTGTTT AAACCCTCAC CACTTGGAGC CCTGGAGCTG CTGTCCCCC AACCCTTGTT 840  
TCCATATGCC GCAGACCCAT AGCCGCCTGC AAGGAAGAGA GGACACAGGA GTAGCCACCC 900  
TGAGTGCCGA CCTTTGGTGG CGGGGGCCTG GGTCTCTCGT CCCCACCCGG AAGGGCACAA 960  
GACACCGGGC TTTGCTTGGC AAGGCTTGGG GCCTCTTGTG GTCAACCCAG TTCCCTTGGG 1020  
TGCCGTTGCA GAACCCCTTA GCCCCTTCCA ACGTCGACCA GGTT 1064

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110 :

AGTTCCTGCA GGTGCCGGCG GTGACGCGGG CTTACACCGC AGCCTGTGTC CTCATCCACC 60  
GCCGCGGTGC AGCTGGAGCT CCTCAGCCCC TTTCAACTCT ACTTCAACCC GCACCTTGTG 120  
TTCCGGAAGT TCCAGGTGAG GCCGCCTCGC GCCGCGCACC TGGGGCCCGA CCCACCCACC 180  
CCGCACCTGA CCGCCCGTCC CCCGTAGGTC TGGAGGCTCG TCACCAACTT CCTCTTCTTC 240  
GGGCCCCCTG GATTTCAGCTT CTTCTTCAAC ATGCTCTTCG TGTATCCTGC GCCTGCGGAC 300  
ACGGGCTGGG TGGAGGGCAG GCCGGCCGGG CTGGGAGAGA GGCCGGGACG GGGAAACTGA 360

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GGCCCCGCCT GGTGGCACTT CCTATACCGA CGCCGTAGGT TCCGCTACTG CCGCATGCTG 420  
GAAGAGGGCT CCTTCCGCGG CCGCACGGCC GACTTCGTCT TCATGTTTCT CTTCGGGGGC 480  
GTCCTTATGA CCGTATCCTT CCCGCAGGCT CTGGAACCTC GGGCTAGGGC GCCTCGGCGT 540  
CCAGCCTGTG TTGGTCTCTG GGCCAACACA GCCATGCCAG AGAGGGACAC AGTCGCTGTC 600  
TCCAGCTTAG CACCGTTCCT GCCTTGGGCG CTCATGGGCT TCTCGCTGCT GCTGGGCAAC 660  
TCCATCCTCG TGGACCTGCT GGGGATTGCG GTGGGCCATA TCTACTACTT CCTGGAGGAC 720  
GTCTTCCCCA ACCAGCCTGG AGGCAAGAGG CTCCTGCAGA CCCCTGGCTT CCTAAAGCTG 780  
CTCCTGGATG CCCCTGCAGA AGACCCCAAT TACCTGCCCC TCCCTGAGGA ACAGCCAGGA 840  
CCCCATCTGC CACCCCCGCA GCAGTGACCC CCACCCAGGG CCAGGCCTAA GAGGCTTCTG 900  
GCAGCTTCCA TCCTACCCAT GACCCCTACT TGGGGCAGAA AAAACCCATC CTAAAGGCTG 960  
GGCCCATGCA AGGGCCCACC TGAATAAACA GAATGAGCTG CAAAAAAAAA AAAAAAGGGC 1020  
GGCCGTCGCG A 1031

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSTUT12
- (B) CLONE: 1812375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111 :

GCTGGATAAG ACACCAGGGG AGTCACTACA TGGTTACCGC ATCTGTATCC AGGCCATCCT 60  
GCAAGACAAG CCAAGATTG CCACGGCAAA CCTAGGCAAG TTCCTGGAAC TGCTGAGGTC 120  
CCACCAGAGC CGACCAGCAA AGTGTCTCAC CATCATGTGG GCCCTGGGTC AAGCAGGTTT 180  
TGCCAACCTC ACCGAGGGAC TGAAAGTGTG GCTGGGGATC ATGCTGCCTG TGCTGGGCAT 240  
CAAGTCTCTG TCTCCCTTTG CCATCACATA CCTGGATCGG CTGCTCCTGA TGCATCCCAA 300  
CCTTACCAAG GGCTTCGGCA TGATTGGCCC CAAGGACTTC TTCCCACTTC TGGACTTTGC 360  
CTATATGCCG AACAACTCCC TGACACCCAG CCTGCAGGAG CAGCTGTGTC AGCTCTACCC 420  
CCGACTGAAA ATGCTGGCAT TTGGAGCAAA GCCGGATTCC ACCCTGCATA CCTACTTCCC 480  
TTCTTTTCTG TCCAGAGCCA CCCCTAGCTG TCCCCCTGAG ATGAAGAAAG AGCTCCTGAG 540  
CAGCCTGACT GAGTGCCTGA CGGTGGACCC CCTCAGTGCC AGCGTCTGGA GGCAGCTGTA 600

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CCCTAAGCAC CTGTCACAGT CCAGCCTTCT GCTGGAGCAC TTGCTCAGCT CCTGGGAGCA 660  
GATTCCCAAG AAGGTACAGA AGTCTTTGCA AGAAACCATT CAGTCCCTCA AGCTTACCAA 720  
CCAGGAGCTG CTGAGGAAGG GTAGCAGTAA CAACCAGGAT GTCGTCACCT GTGACATGGC 780  
CTGCAAGGGC CTGTTGCAGC AGGTTTCAGG TCCTCGGCTG CCCTGGACGC GGCTCCTCCT 840  
GTTGCTGCTG GTCTTCGCTG TAGGCTTCCT GTGCCATGAC CTCCGGTCAC ACAGCTCCTT 900  
CCAGGCCTCC CTTACTGGCC GGTGCTTCG ATCATCTGGC TTCTTACCTG CTAGCCAACA 960  
AGCGTGTGCC AAGCTCTACT CCTACAGTCT GCAAGGCTAC AGCTGGCTGG GGGAGACACT 1020  
GCCGCTCTGG GGCTCCCACC TGCTCACCGT GGTGCGGCCC AGCTTGCAGC TGGCCTGGGC 1080  
TCACACCAAT GCCACAGTCA GCTTCCTTTC TGCCCACTGT GCCTCTCACC TTGCGTGGTT 1140  
TGGTGACAGT CTCACCAGTC TCTCTCAGAG GCTACAGATC CAGCTCCCCG ATTCCGTGAA 1200  
TCAGCTACTC CGCTATCTGA GAGAGCTGCC CCTGCTTTTC CACCAGAATG TGCTGCTGCC 1260  
ACTGTGGCAC CTCTTGCTTG AGGCCCTGGC CTGGGCCCAG GAGCACTGCC ATGAGGCATG 1320  
CAGAGGTGAG GTGACCTGGG ACTGCATGAA GACACAGCTC AGTGAGGCTG TCCACTGGAC 1380  
CTGGCTTTGC CTACAGGACA TTACAGTGGC TTTCTTGAC TGGGCACTTG CCCTGATATC 1440  
CCAGCAGTAG GCCCTGCCTT CCTGGCCACT GATTTCCTGCA TGGGTAGACC ATCCAAGACT 1500  
GCAGCGGGTA GAAGGTGGCA GTTCTTCATG GGAGTCTTTT TAACTTGGTG CCTGAGTTCT 1560  
CTCCTAGGCA AGTGGCCAGT TGCCTCCACC TCAGTTCTTC CATCTTTGGT GGGGACAGGG 1620  
CCCAGCAGCA TCTCAGCCTC CTACCCACAA TTCCACTGAA CACTTTTCTG GCCCTACTGC 1680  
ACATGGCCCC CAGCCTCCAT CCTTGTGCTG GTAGCCTCTC ACAACTCCGC CCTTGCCCTC 1740  
TGCCTTCCAC TTCCTTCCAT CTCATTTCTA AACCCCAAAC AGCTCATCTC TAAAAAGATA 1800  
GAACTCCCAG CAGGTGGCTT CTGTGTTCTT CTGACAAATG ATTCCTGCTT CTCCAGACTT 1860  
TAGCAGCCTC CTGTTCCCAT TCTTGGTCAC AGCTCTAGCC ACAGCAGAAG GAAAGGGGCT 1920  
TCCAGAAGAA TATAGCACCG CATTGGGAAA CAGCAGCCTC ACCTCCACCT GAAGCCTGGG 1980  
TGTGGCTGTC AGTGGACATG GGGAGCTGGA TGGAATGCC TCTCACTTCA AAATGCCCAG 2040  
CCTGCCCCAA ATGCCTCTAA GCCCCTCCCT GTCCCCTCCC TTGTAGTCCT ACTTCTTCCA 2100  
ACTTTCCATT CCCCATCATG CTGGGGGTCT TGGTCACAAG GCTCAGCTTC TCTCCACTGT 2160  
CCATCCCTCC TATCATCTGT AGAGCAGAGC ACAGGCAGTT GTGTGCCTTG GGCCCAGGGA 2220  
ACCCTCCATC AACCTGAGAC AGGACTCAGT ATATGGTTCT TGGGTATGCC CTACCAGGTG 2280  
GAATAAAGGA CACAGATTTG AAAAAAAAAA AAAAAA 2316

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(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT20
- (B) CLONE: 1818761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112 :

AGCAAGGAGC CAGAGGCCAT GCAGTGGCTC AGGGTCCGTG AGTCGCCTGG GGAGGCCACA 60  
GGACACAGGG TCACCATGGG GACAGCCGCC CTGGGTCCCG TCTGGGCAGC GCTCCTGCTC 120  
TTTCTCCTGA TGTGTGAGAT CCCTATGGTG GAGCTCACCT TTGACAGAGC TGTGGCCAGC 180  
GGCTGCCAAC GGTGCTGTGA CTCTGAGGAC CCCCTGGATC CTGCCCATGT ATCCTCAGCC 240  
TCTTCCTCCG GCCGCCCCCA CGCCCTGCCT GAGATCAGAC CCTACATTAA TATCACCATC 300  
CTGAAGGGTG ACAAAGGGGA CCCAGGCCCA ATGGGCCTGC CAGGGTACAT GGGCAGGGAG 360  
GGTCCCCAAG GGGAGCCTGG CCCTCAGGGC AGCAAGGGTG ACAAGGGGGA GATGGGCAGC 420  
CCCGGCGCCC CGTGCCAGAA GCGCTTCTTC GCCTTCTCAG TGGGCCGCAA GACGGCCCTG 480  
CACAGCGGCG AGGACTTCCA GACGCTGCTC TTCGAAAGGG TCTTTGTGAA CCTTGATGGG 540  
TGCTTTGACA TGGCGACCGG CCAGTTTGCT GCTCCCCTGC GTGGCATCTA CTTCTTCAGC 600  
CTCAATGTGC ACAGCTGGAA TTACAAGGAG ACGTACGTGC ACATTATGCA TAACCAGAAA 660  
GAGGCTGTCA TCCTGTACGC GCAGCCCAGC GAGCGCAGCA TCATGCAGAG CCAGAGTGTG 720  
ATGCTGGACC TGGCCTACGG GGACCGCGTC TGGGTGCGGC TCTTCAAGCG CCAGCGCGAG 780  
AACGCCATCT ACAGCAACGA CTTGACACC TACATCACCT TCAGCGGCCA CCTCATCAAG 840  
GCCGAGGACG ACTGAGGGCC TCTGGGCCAC CCTCCCGGCT GGAGAGCTCA GGTGCTGGTC 900  
CCGTCCCCTG CAGGGCTCAG TTTGCACTGC TGTGAAGCAG GAAGGCCAGG GAGGTCCCCG 960  
GGGACCTGGC ATTCTGGGGA GACCCTGCTT CTATCTTGGC TGCCATCATC CCTCCCAGCC 1020  
TATTTCTGCT CCTCTCTTCT CTCTTGACC TATTTTAAGA AGCTTGCTAA CCTAAATATT 1080  
CTAGAACTTT CCCAGCCTCG TAGCCCAGCA CTTCTCAAAC TTGGAAATGC ATGCGAATCA 1140  
CCCGGGGTTC GTGTTAAATG CAGATTCTG 1169

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1530 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: GBLATUT01  
(B) CLONE: 1824469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113 :

TCACAGACTG CGGAGTGGGT CAGGGGCTGC GAGGGCTGCC CCAAGTCCTA CCGGGTTTGC 60  
ACGGGCGCGC CCGGCTCCGC CCGCAAGTGC GCCTTCCTGA CTTACTGCTG GGTGCGCGGG 120  
GCTGGGGGTG CGAGTACCAC CCCTGAAGTC TCTTCCTGGG CGACCTCCGG GGCCTCATTC 180  
TAGGCCCTCCT TAAAGAGAAG GATCTAAATT AGGAAAAGGA AGTGCCCTTA TCCACGACCA 240  
AGCTCTTCCA CCTGCGGAGC TCGCTTAGTC TGCACCTCAA CCGTGCGGAA AGTGA CTGCC 300  
CTGTTTACTG AGGAAAAACT GGGGCTCAGA AAGATACCAT GAGTAGTTTG AAACAGGAAC 360  
AAAATCTTCT GAAAGCTCGG AGCAGAAGCC TTTTGGTCA ACATGGAGGA AAAAAGACGG 420  
CGAGCCCGAG TTCAGGGAGC CTGGGCTGCC CCTGTAAAA GCCAGGCCAT TGCTCAGCCA 480  
GCTACCACTG CTAAGAGCCA TCTCCACCAG AAGCCTGGCC AGACCTGGAA GAACAAAGAG 540  
CATCATCTCT CTGACAGAGA GTTTGTGTTT AAAGAACCTC AGCAGGTAGT ACGTAGAGCT 600  
CCTGAGCCAC GAGTGATTGA CAGAGAGGGT GTGTATGAAA TCAGCCTGTC ACCCACAGGT 660  
GTATCTAGGG TCTGTTTGTA TCCTGGCTTT GTTGACGTGA AAGAAGCTGA CTGGATATTG 720  
GAACAGCTTT GTCAAGATGT TCCCTGGAAA CAGAGGACCG GCATCAGAGA GGATATAACT 780  
TATCAACAAC CAAGACTTAC AGCATGGTAT GGAGAACTTC CTTACACTTA TTCAAGAATC 840  
ACTATGGAAC CAAATCCTCA CTGGCACCCCT GTGCTGCGCA CACTAAAGAA CCGCATTGAA 900  
GAGAACACTG GCCACACCTT CAACTCCTTA CTCTGCAATC TTTATCGCAA TGAGAAGGAC 960  
AGCGTGGA CT GGCACAGTGA TGATGAACCC TCACTAGGGA GGTGCCCCAT TATTGCTTCA 1020  
CTAAGTTTTG GTGCCACACG CACATTTGAG ATGAGAAAGA AGCCACCACC AGAAGAGAAT 1080  
GGAGACTACA CATATGTGGA AAGAGTGAAG ATACCCTTGG ATCATGGTAC CTTGTTAATC 1140  
ATGGAAGGAG CGACACAAGC TGA CTGGCAG CATCGAGTGC CCAAAGAATA CCACTCTAGA 1200  
GAACCGAGAG TGAACCTGAC CTTTCGGACA GTCTATCCAG ACCCTCGAGG GGCACCCTGG 1260  
TGACGTCAGA GCTTTGAGAG AGAAGCTTCA CTGAAACGGA GCAAACCTTC CACTGAGAAG 1320  
CCACTTCAAG AGGCTGGTGC TGCTAGATCT CATGATGTGG CTGTTGGGAA GATGGTGGGG 1380  
TTTGTGTGCC AGCTTGAGT CCTATTAAAT GAAAGCCAGC AACTCATGTT GGTAATAGGT 1440  
CTACTGTGGG AACAGTTATC CCTAACCACA GCTCAAAATC GCTATCATCT TTAGGCAAAT 1500

TAAAATCTAT GTGGCAGTGA AAAAAAAAAA

1530

## (2) INFORMATION FOR SEQ ID NO: 114:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT19
- (B) CLONE: 1864292

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114 :

AGCTCGTACC CCTCGAGTGA AATTCTGAAA TGAAGATGGA GGAGGCAGTG GGAAAAGTTG 60  
 AAGAACTCAT TGAGTCCGAA GCCCCACCAA AAGCATCTGA ACAAGAGACA GCCAAGGAGG 120  
 AAGATGGATC TGTAGAACTG GAATCTCAAG TTCAGAAAAGA TGGTGTAGCG GATTCTACAG 180  
 TTATTTCTTC AATGCCCTGC TTGTTGATGG AACTGAGAAG GGACTCTTCT GAGTCTCAGT 240  
 TAGCATCCAC AGAGAGTGAC AAGCCTACAA CTGGCCGAGT TTATGAGAGT GACCCCTCTA 300  
 ATCACTGCAT GCTTTCCCCT TCCTCTAGTG GTCACCTGGC TGATTGAGAT ACGTTGTCTT 360  
 CCGCAGAAGA GAATGAACCC TCTCAGGCAG AAACGGCGGT AGAAGGAGAC CCTTCAGGAG 420  
 TGTCTGGTGC CACAGTTGGG CGCAAGTCTA GGCGGTCCCG ATCTGAAAGT GAAACTTCCA 480  
 CTATGGCTGC CAAGAAAAAC CGGCAATCCA GTGATAAACA GAATGGCCGA GTCGCCAAGG 540  
 TTAAAGGTCA TCGGAGCCAA AAGCACAAGG AGAGGATCAG GCTACTGAGG CAGAAACGGG 600  
 AGGCTGCTGC AAGGAAGAAA TATAACCTGC TGCAGGACAG TAGTACCAGT GATAGTGACC 660  
 TGACTTGTGA CTCAAGCACG AGCTCATCAG ATGATGATGA AGAGGTTTCA GGGAGCAGCA 720  
 AGACAATCAC TGCAGAGATA CCAGATGGAC CTCCAGTTGT AGCTCATTAT GATATGTCTG 780  
 ACACCAACTC TGACCCAGAA GTGGTAAATG TGGACAATTT ATTGGCGGCT GCAGTAGTTC 840  
 AAGAGCACAG TAATTCTGTA GGCGGCCAGG ACACAGGAGC TACCTGGAGG ACCAGCGGGC 900  
 TTCTAGAGGA GCTGAATGCA GAGGCAGGTC ATTTGGATCC AGGATTCCTA GCAAGTGACA 960  
 AAACATCTGC TGGCAATGCG CCACTCAATG AAGAAATTAA CATTGCGTCT TCAGATAGTG 1020  
 AAGTAGAGAT TGTGGGAGTT CAGGAACATG CAAGGTGTGT TCATCCTCGA GGTGGTGTGA 1080  
 TTCAGAGTGT TTCTTCATGG AAGCATGGCT CGGGCACGCA GTATGTTAGC ACCAGGCAAA 1140  
 CACAGTCATG GACTGCTGTG ACTCCCCAGC AGACTTGGGC TTCACCAGCA GAAGTTGTTG 1200  
 ACCTTACCTT GGATGAGGAT AGCAGGCGTA AATACCTACT GTAATACAAT GTCAGTGTGT 1260

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TTCCTCTGCA CTGTTCCCTT CCACTTCCTC ATCCTCTTTG TGACATGGAA GTTCATTGTC 1320  
ATAGGGGTAC GGAGCT 1336

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1742 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1NOT01
- (B) CLONE: 1866437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115 :

GGCCCGCCCC CTCCCCGCCC GCCTTCCCGG TGACCTTCAG GGGCCCGGGT GGCGGGCGCA 60  
GGCCCCCTGCG GCGGCGGCGG GATGTTTCGTG CAGGAGGAGA AGATCTTCGC GGGCAAGGTG 120  
CTGCGGCTGC ACATCTGCGC GTCCGACGGC GCCGAGTGGC TGGAGGAGGC CACCGAGGAC 180  
ACCTCGGTGG AGAAGCTCAA GGAGCGCTGC CTCAAGCACT GTGCTCATGG GAGCTTAGAA 240  
GATCCCCAAA GTATAACCCA TCATAAATTA ATCCACGCTG CCTCAGAGAG GGTGCTGAGT 300  
GATGCCAGGA CCATCCTGGA AGAGAACATC CAGGACCAAG ATGTCCTATT ATTGAAAAAA 360  
AAGCGTGCTC CATCACCCT TCCAAGATG GCTGATGTCT CAGCAGAAGA AAAGAAAAAA 420  
CAAGACCAGA AAGCTCCAGA TAAAGAGGCC ATACTGCGGG CCACCGCCAA CCTGCCCTCC 480  
TACAACATGG ACCGGGCCGC GGTCCAGACC AACATGAGAG ACTTCCAGAC AGAACTCCGG 540  
AAGATACTGG TGTCTCTCAT CGAGGTGGCG CAGAAGCTGT TAGCGCTGAA CCCAGATGCG 600  
GTGGAATTGT TTAAGAAGGC GAATGCAATG CTGGACGAGG ACGAGGATGA GCGTGTGGAC 660  
GAGGCTGCCC TGCGGCAGCT CACGGAGATG GGCTTTCCGG AGAACAGAGC CACCAAGGCC 720  
CTTCAGCTGA ACCACATGTC GGTGCCTCAG GCCATGGAGT GGCTAATTGA ACACGCAGAA 780  
GACCCGACCA TAGACACGCC TCTTCCTGGC CAAGCTCCCC CAGAGGCCGA GGGGGCCACA 840  
GCAGCTGCCT CCGAGGCTGC CGCGGGAGCC AGCGCCACCG ATGAGGAGGC CAGAGATGAG 900  
CTGACGGAAA TCTTCAAGAA GATCCGGAGG AAAAGGGAGT TTCGGGCTGA TGCTCGGGCC 960  
GTCATTTCCC TGATGGAGAT GGGGTTTCGAC GAGAAAGAGG TGATAGATGC CCTCAGAGTG 1020  
AACAACAACC AGCAGAATGC CGCGTGCGAG TGGCTGCTGG GGGACCGGAA GCCCTCTCCG 1080  
GAGGAGCTGG ACAAGGGCAT CGACCCCGAC AGTCCTCTCT TTCAGGCCAT CCTGGATAAC 1140  
CCGGTGGTGC AGCTGGGCCT GACCAACCCG AAAACATTGC TAGCATTTGA AGACATGCTG 1200



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GAGAACCCAC TGAACAGCAC CCAGTGGATG AATGATCCAG AAACGGGGCC TGTCATGCTG 1260  
CAGATCTCTA GAATCTTCCA GACACTAAAT CGCACGTAGG TGGCGTTGTT CCACTCGGCT 1320  
ATCAGGCCAC AGCAGCCCCC TGGTGCGGCC CGAGACCGGG CAGAGTGGAC CTCACCTGGA 1380  
AACTCACCTT CAGCGCCTCA GCCCTGGACT GTTAGAGGTG CTGCAGCTGC TCCTGCTCTC 1440  
TGATCTTATT GCTTATAAAC TTTGGTGACG GTAGTGTGTA AGGCCGTATT TTTAGCATCT 1500  
GACAGGTGTT TACAAAAAAG TGGTTGTCGC ACTGGGAAGT GGAGTGATGG CCTCGTCTCC 1560  
AGTGCTCCTC TGGGCTCTTG AGTTGCTGCT TGAATTGCCG TGTAGACATT TGCTTGAGAGA 1620  
GTCCACTTGT TATTTGACGG AGGTAGGTTT CAACCCAGAG TTAATGTCAA GCATGCTAAT 1680  
TTAACTAGTC ACTCACAGAT GACTTTTCTT TAATAAAGTC CCTTTTCCTA TAAAAAATA 1740  
AA 1742

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SKINBIT01
- (B) CLONE: 1871375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116 :

GCGGTGCAGA GGAAGCACAA CCTCTACCGG GACAGCATGG TCATGCACAA CAGCGACCCC 60  
AACCTGCACC TGCTGGCCGA GGGCGCCCCC ATCGACTGGG GCGAGGAGTA CAGCAACAGC 120  
GGCGGGGGCG GCAGCCCAGC CCCAGCACCC CGGAGTCAGC CACCCTCTCG GAAAAGCGAC 180  
GGCGCGCCAA GCAGGTGGTC TCTGTGGTCC AGGATGAGGA GGTGGGGCTG CCCTTTGAGG 240  
CTAGCCCTGA GTCACCACCA CTGCGTCCC CGGACGGTGT CACTGAGATC CGAGGCCTGC 300  
TGGCCCAAGG TCTGCGGCCT GAGAGCCCCC CACCAGCCGG CCCCCTGCTC AACGGGGCCC 360  
CCGCTGGGGA GAGTCCCCAG CCTAAGGCCG CCCCCGAGGC CTCCTCGCCG CCTGCCTCAC 420  
CCCTCCAGCA TCTCCTGCCT GGAAAGGCTG TGGACCTTGG GCCCCCAAG CCCAGCGACC 480  
AGGAGACTGG AGAGCAGGTG TCCAGCCCCA GCAGCCACCC CGCCCTCCAC ACCACCACCG 540  
AGGACNANTT TCAAGGGGTG CAAGAATTGA AGNTTCNTAA GGGCCAANTT GGGGGTCCCC 600  
TTGACTTGGN TTGGNAANAT TGGGGCAAAA AGGGCCGGTT TTCCCNTTT CCCGGGANAC 660  
CCCAAGGGAA AGGGGNTTCA AAGCTTCTTN GGGGGGGAAA GGGGGAANCC CTTGGGTNTT 720

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TTGTTGGCCN TTTGTGANCA NCAGCGAGGA GAGTGCAAAG GTGCAGAGTN AGTTNTAGGN 780  
CANTGGGTCC CTGACTGCTG CANATGGTAA GGNCGTNNC TTGTGGACCC AAGGCAGGNA 840  
AAGNTGTGGG GAGGGAAGCT GGTNTGTGCN TTGTGGGTGG AAGCGGGGAN GGCTGTGTTG 900  
NANGGCAGGG AGAGGGCNAA NTGAGTTATT TATTGGGGTT CANGTGAAAA GTTTCTTGNN 960  
CCCTGTNTTG TGTNCTGTG GGATTGATTN TAAGATNGNN AGGGGTNGGT TTTTGGGGTT 1020  
TTCCTGGTTG GTGGCCAAAN GGGTTGGAAA ATNGNTGGGG GGGGNTTGGA NAAT 1074

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LEUKNOT03
- (B) CLONE: 1880830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117 :

CCCGGGGGAG GCCTGACCCC CTCCGCACCA CCGTACGGAG CCGCATTTCC CCCGTTTCCC 60  
GAGGGGCATC CAGCCGTGTT GCCTGGGGAG GACCCACCCC CCTATTCACC CTTAACTAGC 120  
CCGGACAGTG GGAGTGCCCC TATGATCACC TGCCGAGTCT GCCAATCTCT CATCAACGTG 180  
GAAGGCAAGA TGCATCAGCA TGTAGTCAAA TGTGGTGTCT GCAATGAAGC CACCCCAATC 240  
AAGAATGCAC CCCAGGGAA AAAATATGTT CGATGCCCCT GTAAGTGTCT CCTTATCTGC 300  
AAAGTGACAT CCCAACGGAT TGCATGCCCT CGGCCCTACT GCAAAAGAAT CATCAACCTG 360  
GGGCCTGTGC ATCCCGGACC TCTGAGTCCA GAACCCCAAC CCATGGGTGT CAGGGTTATC 420  
TGTGGACATT GCAAGAATAC TTTTCTGTGG ACAGAGTTCA CAGACCGCAC TTTGGCACGT 480  
TGTCTCACT GCAGGAAAGT GTCATCTATT GGGCGCAGAT ACCCACGTAA GAGATGTATC 540  
TGCTGCTTCT TGCTTGGCTT GCTTTTGGCA GTCAGTCCA CTGGCCTTGC CTTTGGCACA 600  
TGGAAGCATG CACGGCGATA TGGAGGCATC TATGCAGCCT GGGCATTGT CATCCTGTTG 660  
GCTGTGCTGT GTTTGGGCCG GGCTCTTTAT TGGGCCTGTA TGAAGGTCAG CCACCCTGTC 720  
CAGAACTTCT CCTGAGCCTG ATGACCCACA GACTGTGCCT GGCCCTCCC TGGTGGGGAC 780  
AGTGACACTA CGAAGGGAGC TGGGGTAGTT AAAGGCTCCC GGGGCTTCTA GAAGGAAGCC 840  
AAGCAGCTGC CTTCTTTTC CCTGGGGAGA GGTAGGAAGG AACCAGGCCC TCACTTAGGT 900  
TTGGAGGGGC AGATAAGAGC ACTGCTGACC ATCTGCTTTC CTCCAAGGGT TGCTGTGTCT 960

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AGGGTGAAGT AGGCAAAACG TTGCCCTTAA AACTGGGCCC TGAAGACGGT TCCAGCCTTG 1020  
TCCTTCCTGT GTGCTCCCTG AGAGCCATTC CTGTCCCTTA CACATTCCAG GGCAGGGTGG 1080  
GGGTGGGTAG CCCTGGGGGT TCCCCTCCCT CTTGTGCACC ATTAGGACTT TGCTGCTGCT 1140  
ATTGCACTTC ACCAGAGGTT GGCTCTGGCC TCAGTACCCT CAGTCTCCTC TCCCCACATT 1200  
GTGTCCTGTG GGGGTGGGGT CAGCCGCTGC TCTGTACAGA ACCACAGGAA CTGATGTGTA 1260  
TATAACTATT TAATGTGGGA TATGTTCCCC TATTCCTGTA TTTCCCTTAA TTCCTCCTCC 1320  
CGACCTTTTT TACCCCCCA GTTGCAGTAT TTAAGTGGGC TGGGTAGGGT TGCTCAGTCT 1380  
TTGGGGGAGG TTAGGGACTT ATCCTGTGCT GTAAATAAA TAAGGTCATG ACTCTAAAAA 1440  
AAAAAAAAGG GCGG 1454

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2071 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARNOT07
- (B) CLONE: 1905325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118 :

AGCTTTGAAT TCCTGTATCT GAGAACGGAT CGTTCGAGGT GGTGGAGGGG GTTGAATTG 60  
GGGACCTACG GAAGGCTCAG CTCTTGCCAG GCCAAATTGA GACATGTCTG ACACAAGCGA 120  
GAGTGGTGCA GGTCTAACTC GCTTCCAGGC TGAAGCTTCA GAAAAGGACA GTAGCTCGAT 180  
GATGCAGACT CTGTTGACAG TGACCCAGAA TGTGGAGGTC CCAGAGACAC CGAAGGCCTC 240  
AAAGGCACTG GAGGTCTCAG AGGATGTGAA GGTCTCAAAA GCCTCTGGGG TCTCAAAGGC 300  
CACAGAGGTC TCAAAGACCC CAGAGGCTCG GGAGGCACCT GCCACCCAGG CCTCGTCTAC 360  
TACTCAGCTG ACTGATACCC AGGTTCTGGC AGCTGAAAAC AAGAGTCTAG CAGCTGACAC 420  
CAAGAAACAG AATGCTGACC CGCAGGCTGT GACAATGCCT GCCACTGAGA CCAAAAAGGT 480  
CAGCCATGTG GCTGATACAA AGGTCAATAC AAAGGCTCAG GAGACTGAGG CTGCACCCTC 540  
TCAGGCCCCA GCAGATGAAC CTGAGCCTGA GAGTGCAGCT GCCCAGTCTC AGGAGAATCA 600  
GGATACTCGG CCAAGGTCA AAGCCAAGAA AGCCCGAAAG GTGAAGCATC TGGATGGGGA 660  
AGAGGATGGC AGCAGTGATC AGAGTCAGGC TTCTGGAACC ACAGGTGGCC GAAGGGTCTC 720  
AAAGGCTCTA ATGGCCTCAA TGGCCCGCAG GTTCAAGGG GTCCCATAGC CTTTTGGGCC 780

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CGCAGGATTC AAGGACTCGG TTGGCTGCTT GGGCCCGGAG AGCCTTGCTC TCCCTGAGAT 840  
CACCTAAAGC CCGTAGGGCA AGGCTCGCCG TAGAGCTGCC AAGCTCCAGT CATCCCAAGA 900  
GCCTGAAGCA CCACCACCTC GGGATGTGGC CCTTTTGCAA GGGAGGGCAA ATGATTTGGT 960  
GAAGTACCTT TTGGCTAAAG ACCAGACGAA GATTCCCATC AAGCGCTCGG ACATGCTGAA 1020  
GGACATCATC AAAGAATACA CTGATGTGTA CCCCAGAAATC ATTGAACGAG CAGGCTATTC 1080  
CTTGAGAGAAG GTATTTGGGA TTCAATTGAA GGAAATTGAT AAGAATGACC ACTTGATACAT 1140  
TCTTCTCAGC ACCTTAGAGC CCACTGATGC AGGCATACTG GGAACGACTA AGGACTCACC 1200  
CAAGCTGGGT CTGCTCATGG TGCTTCTTAG CATCATCTTC ATGAATGGAA ATCGGTCCAG 1260  
TGAGGCTGTC ATCTGGGAGG TGCTGCGCAA GTTGGGGCTG CGCCCTGGGA TACATCATTC 1320  
ACTCTTTGGG GACGTGAAGA AGCTCATCAC TGATGAGTTT GTGAAGCAGA AGTACCTGGA 1380  
CTATGCCAGA GTCCCCAATA GCAATCCCCC TGAATATGAG TTCTTCTGGG GCCTGCGCTC 1440  
TTACTATGAG ACCAGCAAGA TGAAAGTCCT CAAGTTTGCC TGCAAGGTAC AAAAGAAGGA 1500  
TCCCAAGGAA TGGGCAGCTC AGTACCGAGA GGCGATGGAA GCAGATTTGA AGGCTGCAGC 1560  
TGAGGCTGCA GCTGAAGCCA AGGCTAGGGC CGAGATTAGA GCTCGAATGG GCATTGGGCT 1620  
CGGCTCGGAG AATGCTGCCG GGCCCTGCAA CTGGGACGAA GCTGATATCG GACCCTGGGC 1680  
CAAAGCCCGG ATCCAGGCGG GAGCAGAAGC TAAAGCCAAA GCCCAAGAGA GTGGCAGTGC 1740  
CAGCACTGGT GCCAGTACCA GTACCAATAA CAGTGCCAGT GCCAGTGCCA GCACCAGTGG 1800  
TGGCTTCAGT GCTGGTGCCA GCCTGACCGC CACTCTCACA TTTGGGCTCT TCGCTGGCCT 1860  
TGGTGGAGCT GGTGCCAGCA CCAGTGGCAG CTCTGGTGCC TGTGGTTTCT CCTACAAGTG 1920  
AGATTTTAGA TATTGTTAAT CCTGCCAGTC TTTCTCTTCA AGCCAGGGTG CATCCTCAGA 1980  
AACCTACTCA ACACAGCACT CTAGGCAGCC ACTATCAATC AATTGAAGTT GACACTCTGC 2040  
ATTAAATCTA TTTGCCATTT CAAAAAAAAA A 2071

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT01
- (B) CLONE: 1919931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119 :

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ACCTGGGACC CCCAGAACGG CCGCCCCTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT 60  
TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTAG AAGGTTGAAA CCAGGCTTAT 120  
TTATTTTCAT CTTCTTTCTG CCATCTTTTA ACCAACCTTC TCAGAATAAA ATGTGATTTT 180  
TGAGACAGAA TGAAACACAT ATCCAAATTT TAATACAGTA AGAATAGGTA TCCTGAATAA 240  
ATGAGAACTC TAGAAAATCA AGGTTTCAAA ATTCTACCCT TCCTGGGAGT TAAAGAAGTT 300  
TGGCAGAAAC AGAACAAATT AATCAGCAGA TTCATCACCT GCCAATTTTT TCTGTACAAT 360  
TTTCTTGATT CTGGGAGCAT CTGGGTCCAG GCAGATTTTC CTCCCATCCT TCAGTGTGGC 420  
TGCTTCTTGT TTCATCCATG GACCCTGCAA GAAATTGCCC CATGTTTCTG TTTGTGCATC 480  
ACTGAGAAAG GAAGCATGAA GGTGCGACAG GTCAGGCCAT TCCATTGCCC TCCTGGTGCC 540  
GGGTTTGCCC TCCCAATCCT GGGGTTGCTT CAGGGGCTTG TCATTCTCCA TAGTCCCCTC 600  
CACATTTCTC AGGTTTCTGC TCAAAAGTCA CCTTTTGAG GGGTCTCCAC CTGTCACTGT 660  
GTTTGTAAGA GCTCCTTCAG TTTCTTTCTA GCTCATCTCA CTCTGGTAAT GTCTTTGATT 720  
ACCACCACCA TCTGACCTGG TCTTATGACC TGTTAGCTTT CTTATCAGA CGTGAGCACC 780  
AGGATGGCAG GGGCCTCATC TGTCTGTTC CTCCTGTGGC CTGGGTCCTA GCACCATGTC 840  
TGGTACAGTG TAGATGCTCA AGGGAAGTTT ACTTTGTAAA ACCACTTACC TGGGAGATGT 900  
TACTGTTAGT CTAACCTGTA CCATTTTGTA AACCTCCAGC CATTTTGAG ACTCTGATCA 960  
CAGTGAAACG TTCCATGGGA ACTTGGGCCA TGAGAAACAT CCTTCCTAAC CACGTGACTG 1020  
CAGAAACATC CTTATCGCGT CCTCCTGGGC AAAGGCCCAA CAGCCTGACT GCAGGGACAT 1080  
CCTTGCCATA TCCTGCTGGG CAGCAAGCTC TACCACCCAG ATCCCTCCCT CCCAGTCCCA 1140  
TGATTACCCC AGCCTGTGAG TGGCAGTTGG TGCTGGCACT AAGCTGGTTT CCTCCTCCCC 1200  
AGGGTTTTCG TGGCAATAAA GATGTTGCTG TTGAAG 1236

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT04
- (B) CLONE: 1969426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120 :

GTACTGCCCA CCACCTCCCT GGGCCACCCC TCACTCAGTG CTCGGGCTCT CTCCTCCTCC 60

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TCTTCGTCCT CCTCCACTTC ATCTCCTGTT TTGGGCTCCC CCTCTTACCC TGCTTCTTCC 120  
CCTGGGGCCT CCCCCACCA CCGCCGTGTG CCCCTCAGCC CCCTGAGTTT GCTCGCGGGC 180  
CCAGCCGACG CCAGAAGGTC CCAACAGCAG CTGCCCCAAC AGTTTTCGCC AACAAATGTCA 240  
CCCACCTTGT CTTCCATCAC TCAGGGGCGTC CCCCTGGATA CCAGTAAACT GTCCACTGAC 300  
CAGCGGTTAC CCCCATACCC ATACAGCTCC CCAAGTCTGG TTCTGCCTAC CCAGCCCCAC 360  
ACCCCAAAGT CTCTACAGCA GCCAGGGCTG CCCTCTCAGT CTTGTTCAGT GCAGTCCTCA 420  
GGTGGGCAGC CCCCAGGCAG GCAGTCTCAT TATGGGACAC CGTACCCACC TGGGCCCAGT 480  
GGGCATGGGC AACAGTCTTA CCACCGGCCA ATGAGTGACT TCAACCTGGG GAATCTGGAG 540  
CAGTTCAGCA TGGAGAGCCC ATCAGCCAGC CTGGTGCTGG ATCCCCCTGG CTTTTCTGAA 600  
GGGCCTGGAT TTTTAGGGGG TGAGGGGCCA ATGGGTGGCC CCCAGGATCC CCACACCTTC 660  
AACCACCAGA ACTTGACCCA CTGTTCCCGC CATGGCTCAG GGCCTAACAT CATCCTCACA 720  
GGGGACTCCT CTCCAGGTTT CTCTAAGGAG ATTGCAGCAG CCCTGGCCGG AGTGCCTGGC 780  
TTTGAGGTGT CAGCAGCTGG ATTGGAGCTA GGGCTTGGGC TAGAAGATGA GCTGCGCATG 840  
GAGCCACTGG GCCTGGAAGG GCTAAACATG CTGAGTGACC CCTGTGCCCT GCTGCCTGAT 900  
CCTGCTGTGG AGGAGTCATT CCGCAGTGAC CGGCTCCAAT GAGGGCACCT CATCACCATC 960  
CCTCTTCTTG GCCCCATCCC CCACCACCAT TCCTTTCCTC CCTTCCCCCT GGCAGGTAGA 1020  
GACTCTACTC TCTGTCCCCA GATCCTCTTT CTAGCATGAA TGAAGGATGC CAAGAATGAG 1080  
AAAAAGCAAG GGGTTTGTCC AGGTGGCCCC TGAATTCTGC GCAAGGGATG GGCCTGGGGG 1140  
AACTCAAGGG AGGGCCTAAA GCACTTGTA CTTTGAACCG TCTGTCTGGA GGTCAGAGCC 1200  
TGTTGGAAAG CAGGGGTAGA GGGGAGCCCT GGAAGCAGGG CTTTTCCGGA TGCCTAGGGG 1260  
TGGGCAGTGC CAGCCCCTCC TCACCACTCT TCCCCTTGCA GTGGAGGAGA GAGCCAGAGT 1320  
GGATACTATT TTTTATTAAA TATATTATTA TATGTTAATA AAAAAATCAT ATCAAAAAAA 1380  
AAAAAAAAG G 1391

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UCMCL5T01
- (B) CLONE: 1969948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121 :

CTCTGTGAAC ATATGATGAG AGAAGCCAAG ATCATGCAGT ATAAGTACCT ACTGTTTCAGT 60  
 CTTACACGCCA TAGTGAAGCT TGGAATCCCT CAGAACACTA TTTTGGTGCA GACTTTGCTG 120  
 AGGGTGACCC AGGAACGTAT CAATGAGTGT GATGAGATAT GCCTTTCAGT TTTGTCAACT 180  
 GTTTTAGAGG CAATGGAACC ATGCAAGAAT GTTCATGTTC TACGAACGGG ATTCAGAATA 240  
 CTAGTTGATC AGCAAGTTTG GAAATAGAA GATGTCTTCA CATTACAAGT TGTGATGAAG 300  
 TGTATTGGAA AAGATGCACC GATTGCTCTT AAGAGGAAAC TGGAGATGAA AGCCTTGAGG 360  
 GGATTAGACA GATTTTCTGT TTTGAATAGC CAACACATGT TTGAAGTACT AGCTGCCATG 420  
 AATCACCAGT CTCTTATACT CCTGGATGAA TGCAGTAAGG TGGTCCTAGA TAATATCCAT 480  
 GGGTGTCCCT TAAGAATAAT GATCAACATA TTGCAGTCCT GCAAAGACCT CCAGTACCAT 540  
 AATTTGGATC TCTTCAAGGG ACTTGCAGAT TATGTGGCTG CAACTTTCGA CATCTGGAAG 600  
 TTCAGAAAAG TTCTTTTTAT CCTCATTTTA TTTGAAAACC TTGGCTTTCG ACCTGTTGGT 660  
 TTAATGGACC TGTTTATGAA GAGAATAGTA GAGGATCCTG AATCCCTAAA CATGAAAAAC 720  
 ATTCTATCTA TTCTTCATAC TTAATCTTCT CTCAATCATG TCTACAAATG CCAGAACAAA 780  
 GAACAGTTCG TGGAAGTTAT GGCTAGTGCT CTGACTGGTT ATCTTCACAC TATTTCTTCT 840  
 GAAAACTTAT TGGATGCAGT ATATTCATTT TGCTTGATGA ATTACTTTCC CCTGGCTCCT 900  
 TTTAATCAGC TTCTGCAAAA AGACATCATC AGTGAGCTGC TGACATCAGA TGACATGAAG 960  
 AATGCTTACA AGCTGCATAC TTTGGATACT TGTCTAAAAC TTGATGATAC TGTCTATCTG 1020  
 AGGGACATAG CCTTGTCCT CCCACAGCTG CCGCGGGAGC TGCCATCGTC ACATACAAAT 1080  
 GCAAAGGTGG CAGAGGTGCT GAGCAGCCTT CTGGGAGGTG AAGGACACTT CTCAAAGGAT 1140  
 GTGCACTTGC CACACAATTA TCATATTGAT TTTGAAATCA GAATGGACAC TAACAGGAAT 1200  
 CAAGTGCTAC CACTTTCTGA TGTGGATACA ACTTCTGCTA CAGATATTCA AAGAGTAGCT 1260  
 GTGCTATGTG TTTCCAGATC TGCTTATTGT TTGGGTTCAA GCCACCCAG AGGATTCCTT 1320  
 GCTATGAAAA TGCGGCATTT GAATGCAATG GGTTTTCATG TGATCTTGGT CAATAACTGG 1380  
 GAGATGGACA AACTAGAGAT GGAAGATGCA GTCACATTTT TGAAGACTAA AATCTATTCA 1440  
 GTAGAAGCTC TTCCTGTTGC TGCTGTAAAT GTGCAAAGCA CACAATAAAG TGAAAATCAA 1500  
 CCTTTTCATA TTAGGAGACA TGCATTTGTA AAAATTAATA AAGATGACAA GTCAGTTGTC 1560  
 AATGGAATTG AGCTATCTGC TAAGACAAAA AATGTTACCT CAGTTCCTA TTAAAATTAA 1620  
 TTTTAGGAGT GGAAGAAATG TTGTTACTGC CATTTAAAAA TATGCTGAGA AAATTCCAGA 1680  
 AGGGTTATTT TTCCAACCAC ACCTATTCCC TCTAGTGCCC AGATATTTGA TTTGTGAGCT 1740  
 GTACGTTTCA CCTTTTCATC TTTGATCTAC TAAAACTGG TTTCTTAGTT GTGAGGTGTC 1800

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ACAGGCAGGT TGATGTGGGT AGTAGTCCTT GTCTTTGGAA TCTGAATATT TATACTCCTG 1860  
CTCTAAGCTG TTCTAAGACT TGGGGTTATG CCTTTAAATC ATTTTCAAGC ATTGGCCAAA 1920  
TAATAATTGG ACAAAGTTCT AAAGTTGTCA AGTGTGTAAG AATTAGTGAG GTAGCTGTTG 1980  
AAAATGAGTG AGGATGGTAT TTGTATTTGT AATAAGCACT GCAGGTAGAG ATATTTTCATG 2040  
GGTTATAATA AGAGAAACAC AGATGAGATG TAGATGGTAA GGAGTCTTAC TGTTGTTGGG 2100  
GTCCTTCCTT TCTCTTTCTT TTTTCCCCCT TACCCCTCCC ACAATTTTCAT GAAGTCTTTT 2160  
AAATTAAATA TATAGCTTNA ATT 2183

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2066 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGAST01
- (B) CLONE: 1988911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122 :

AGAACCACTG CAGTGGAGAC TCCATGTGCA AAAGAAAAAA ACCAAATGTG AGGTCATAAA 60  
GACTTTCTGC CAGCATGTGG GTGACATTGT TTCTTTGCAG ATTTTGGCTA TGGAAAGGGG 120  
AAATGTTCTA AGCAGAGCCC CGTCAAGAGC CCACGGGACA CATTTTGGAG ATGACAGATT 180  
TGAAGATCTG GAAGAGGCAA ATCCATTCTC TTTTAGAGAG TTTCTGAAGA CCAAGAACCT 240  
CGGCCTCTCG AAAGAGGATC CGGCCAGCAG AATTTATGCA AAGGAAGCCT CGAGGCATTC 300  
CCTGGGACTT GACCACAACT CCCCACCCTC CCAAACCGGC GGGTATGGCC TGGAGTATCA 360  
GCAGCCATTT TTCGAGGATC CGACAGGGGC TGGTGACCTC CTGGATGAGG AGGAGGATGA 420  
GGACACCGGA TGGAGTGGGG CCTACCTGCC GTCCGCCATC GAGCAGACTC ACCCCGAGAG 480  
GGTCCCTGCC GGCACGTCGC CCTGCAGCAC ATACCTTTCC TTTTCTCCA CCCCCTCGGA 540  
GCTGGCAGGG CCTGAGTCTC TGCCCTCGTG GGCGTTGAGT GACACTGATT CTCGCGTGTC 600  
TCCGGCCTCT CCGGCAGGGA GTCCTAGCGC AGACTTTGCG GTTCATGGAG AGTCTCTGGG 660  
AGACAGGCAC CTGCGGACGC TGCAGATAAG TTACGACGCA CTGAAAGATG AAAATTCTAA 720  
GCTGAGAAGA AAGCTGAATG AGGTTCAGAG CTTCTCTGAA GCTCAAACAG AAATGGTGAG 780  
GACGCTTGAG CGGAAGTTAG AAGCAAAAAT GATCAAGGAG GAAAGCGACT ACCACGACCT 840  
GGAGTCGGTG GTTCAGCAGG TGGAGCAGAA CCTGGAGCTG ATGACCAAAC GGGCTGTAAA 900



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GGCAGAAAAC CACGTCGTGA AACTAAAACA GGAAATCAGT TTGCTCCAGG CGCAGGTCTC 960  
CAACTTCCAG CGAGAGAATG AAGCCCTGCG GTGCGGCCAG GGTGCCAGCC TGACCGTGGT 1020  
GAAGCAGAAC GCCGACGTGG CCCTGCAGAA CCTCCGGGTG GTCATGAACA GTGCACAGGC 1080  
TTCCATCAAG CAACTGGTTT CCGGAGCTGA GACACTGAAT CTTGTTGCCG AAATCCTTAA 1140  
ATCTATAGAC AGAATTTCTG AAGTTAAAGA CGAGGAGGAA GACTCTTGAG GACCCCTGGG 1200  
TGTTCTCAGC ATGAAGCTCC GTGTATACCC TGAGGTCACC ACCGCTCGAT CTAAATGTGC 1260  
AGTTGTGTCC TTAAATATGC AGTCTTCACC CAGAGTAAAG TGTGATCGC AAGAGTCCAG 1320  
TGTCGTGCCC TCAGCCAGTT CTTGGCCACC ACAATGGGAG CAGCCCTGGC CGAGTTGTCT 1380  
CTGTGGTTTC TATGCAGCCC TTCTTGCGCA AATTCCTGCG ATCTTATAGA TTCTAATGAG 1440  
CTCTTGGAAG ACATTGTCAT AAAAGCCAGT GATTTTAAGA AAAAGAGTGG TTCTGGAATC 1500  
AATGTTTTCC AGTCCCATCC CAGAACATCA GTTGTAAGAT AAGTACAATT GGTTGTCCTT 1560  
GATTTTCATAA GTAGAACAAA CACTAAATGT GCCTCTGAGA TGGCCACCCC GGGCAGGGAC 1620  
CTGTGCCTTC CGCCGATGCT CAGGGCTCCC TCTGGCTCCC GGGTCACTCT TGTGGCCCCA 1680  
GTGGGTGGTC CCTGCAGTCA TGGCCTGAGT GCGCAGGGGC CACCGCGTGG CTGCTGCTGT 1740  
CCTCCTCCGG GACCCACGGG GACCAAGGTC ACACGTCCG TGCTGTGAAG CTGTCCAGAT 1800  
GTGCCTCTTT GGCTGGGGGT TCTGGTGGAC GTTTCAAGTG GCATTTTGTA CAATGCAGGT 1860  
TAGAATTCAG GAATTTCAAG TATGTGCCCG GGTCTGTCAG GTCCCAGTTG CCTTTCTGAC 1920  
GGCCCCCTC AGAGGGACGG CGATGAGCAC TAAATGCTTT TTTGACTATT TTCCTATAGA 1980  
TTTTTTTTTAA AACTTTTTTT TCCTCCTGTT CCAATTGATA GCTTTCTTAT TTAATAAATT 2040  
CTGTAGTTCA CCGCAAAAAA AAAAAA 2066

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1867 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARNOT03
- (B) CLONE: 2061561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123 :

TGGCCAGGCT GGTCTAGAAC TCCTGACTGC AAATGATCAG CCCGCCTCAG CCACCCAAAG 60  
TGTGTTGGGATT ACAGGTGTGA GCCACTGTGC CCAGCGTGAT TTTTTTTTTT TTAAAGCAA 120

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ACTTGTCCCTT TGGTTTTGCA GAACAGGCCT GCTCCCTCTC ATCTAGCCCA TCATTTCTTG 180  
GGGCCTGAAC CCCAGTGGTC CAAAGTATTG CTTGTGAAAT TTAAAAAATG TGAATATGAT 240  
GTGGGGATGG GCCTCTTCTA CATTACCTTG GCCCAGGGGG ATCAGCTGGC TGGGAGGATT 300  
AGTGAGCACC TCTGTATTTT GAGGTCTGAG TCTTCTGGAG CTGTGTAGTT AATCTTCGGT 360  
TTCTGATAAC CCCTGGGTCC ATCTGGCCAT CAGCCTCAGC AGTGAGCAAA GCAATACCAT 420  
ACTCATTTCT ATGTTCCCTGT TCCTTCCTCT GCTCCTCCTT TGGAGAAGCA ATAATTCATG 480  
GGGGATGATA CAGTAGCACT TTACAAATGG CTCCATGTCA TTCATCCCAG GGGCCATAAT 540  
CTCTTGACACC ACCTATTCTT ACTTCCTGTT CAGCTCCTTT ACAGCTTTTA TTTTCAACTG 600  
CTTCCCAACT TGGTGGGGCC TCCTTTAAGG ATGAGCCAAT AGTAAGAATG TGGCTGTAAT 660  
CAGCAGAGAC CCCTCTGAGG GGTATCTGTT CTGCAGCCCC TAGTGAAATC ATGTGATGTG 720  
AGACAGAAAC CTAAACATGG TACTTGATTG TAAACCTGTG CCAGTCTATA GCCTCTGCCT 780  
CCCCAAGCAG AGCTCAAGCC AAACGCTTCT GTCTCTTTTC CTTCTGCATT AACCCTTTGC 840  
TGATCCTCAG GGGCCACTCC CCCAACACCC CTGTACTTGG GTGAGGGATG TTGGACAGAG 900  
CCTGTTTTCA TGTACTGCAG GTGGGGGTGT GCTGACATGT TTGCTCTTGG TTGATGGAGA 960  
AGGTACAGAG GCCAGGGAGT GAAAATGGTT GACAGAAGAG GGAAGAGTTA GGTGTCTCAT 1020  
AGTCACTCAT AGTGGGGTGG TCAGGGGTAA TGGCATCTCC CCACTTTAGG CTTCTCAAAC 1080  
AGACTTTTGA CACCTCTCAA GTTCAGAGCT CTGATGTGGA AAGACAGGAG GTGTGGGGAA 1140  
GGAGGGGGAT TTCGTGTGTT TGCATGAGTG TGCGCTTCAG GCCTTGGGAG TTGGCAAGAG 1200  
GGAGGGAAGG AAGGAGAGCA AAATCTTCGG AAGGTGTTTC TTGTACCTGA GGGATCCTGC 1260  
CCTGAATCTC CATAGTCTCC ACTGTGAACT GAGGAGGGGA GGGGTGTGCT GGGGAATAAA 1320  
TCTTGTATGA GAACAATCAA AAATCAAACG AATCCCACCG ACAGACTGCT GCTCCTAGTG 1380  
ATCTGGACTC ACCTAGGGGG CATCTGGGCT GGGGTTCAN GCTTACGTNC GCGTGNATGN 1440  
GACGNCANAG CTCTTCGAAA GTGTCCCNAA ANTNC AATTC ATTGGCGGTG GTTTTAAAAG 1500  
TTCGGGCCTG GGAAACCCGG GGGNTTACCC ATTTTATCCC NCTTNGANGG CANATTCCCC 1560  
TTTTTCCCCA ATTTGGGGAA ATTTNCCAAA NGGGNCCCGT AACGGTTGGC CTTTTCCCAA 1620  
AATTTNGGNC GCCCTTAATT GGGGCGATTG TGGGACCCGC GCCCTTTATA GGGGGGGGCT 1680  
TTAAAGCGGC GCNNGGGGTT CTTTGGGTGA TTACCGGCGC GGTTGACCCC GGGTAAAATA 1740  
TTGACAAGGG CCCTTTAGCG CGCGGTTCTT TGTGGGGTTT TCCTCCCAT TGTCTTTTCC 1800  
GCAAAAGTTT TGGCGGGGTT TTCCCCGGAA AAGGTCTTAA AAAGCGGTGT GCCCCTCTTT 1860  
GAGGGGG 1867

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PANCNOT04
- (B) CLONE: 2084489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124 :

CTCTGGGTCT GTAGCAACCG CCCAGCGTTG AGGCGCGGCT CATGCCCCCA GTATCCCGGT 60  
 CCAGCTATTC CGAGGACATC GTGGGCTCTC GGAGAAGGCG ACGCAGCTCC TCGGGGAGCC 120  
 CACCATCCCC GCAGAGCAGA TGTTCTCTCTT GGGATGGCTG TTCCCGCTCT CACTCCCGCG 180  
 GCCGTGAGGG CCTCAGGCCT CTTTGGAGTG AGTTGGACGT GGGCGCTCTT TACCCCTTTA 240  
 GTCGCTCTGG GTCGCGAGGG CGGCTCCCAA GATTCCGCAA CTACGCCTTC GCGTCCTCCT 300  
 GGTCGACCTC GTATAGTGA TATCGCTACC ATCGTCACTG CTATGCAGAA GAACGGCAGT 360  
 CAGCGGAAGA CTACGAGAAG GAAGAGAGCC ATCGGCAGAG GAGGCTGAAG GAGAGAGAGA 420  
 GGATTGGGGA ATTGGGAGCG CCTGAAGTGT GGGGGCCGTC TCCAAAGTTC CCTCAGCTAG 480  
 ATTCTGACGA ACATACCCCA GTTGAGGATG AAGAAGAGGT AACGCATCAG AAAAGCAGCA 540  
 GTTCAGATTC CAACTCGGAA GAACATAGGA AAAAGAAGAC CAGTCGTTCA AGAAACAAGA 600  
 AAAAAAGAAA GAATAAGTCG TCTAAAAGAA AGCATAGGAA ATATTCTGAT AGTGACAGTA 660  
 ACTCAGAGTC TGACACAAAT TCTGACTCTG ATGATGATAA AAAGAGAGTT AAAGCCAAGA 720  
 AGAAAAAGAA GAAAAAGAAA CACAAAACAA AGAAAAAGAA GAATAAGAAA ACCAAAAAAG 780  
 AATCCAGTGA CTCAAGCTGT AAAGACTCAG AAGAGGACTT GTCAGAAGCT ACCTGGATGG 840  
 AGCAGCCAAA TGTGGCAGAT ACTATGGATT TAATAGGGCC AGAAGCACCT ATAATACATA 900  
 CCTCTCAAGA TGAAAAACCT TTGAAGTATG GCCATGCTTT GCTTCCCGGT GAAGGTGCAG 960  
 CTATGGCTGA GTATGTAAAA GCTGGAAAGC GAATCCCACG AAGAGGTGAA ATTGGGTTGA 1020  
 CAAGTGAAGA GATCGGTTCT TTTGAATGCT CAGGTTATGT CATGAGTGGT AGCAGGCATC 1080  
 GCAGAAATGA GGCTGTACGA CTGCGTAAGG AGAACCAGAT CTACAGTGCT GATGAGAAGA 1140  
 GAGCTCTTGC ATCCTTTAAC CAAGAAGAGA GACGAAAGAG AGAAAGTAAG ATTTTAGCCA 1200  
 GTTTCGAGA GATGGTGCAC AAAAAGACAA AAGAGAAAGA TGACAAGTAA GGACTTACTT 1260  
 GTTGCACAGC AGGAATTTTA ACAACAAAAA TTTTATGTGA CCAAAGTGT TAAAAGGCTT 1320  
 TACAGTGCTA CTGTACTTAC CATATTAGTA AGTCCCTCAG GAAAAAGCTT CTTTTGAGAT 1380

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ATCTTTAGCA GCTTATTTTT TGTTATTTTA ACTTTAAAAA GTAATATGTG CACATGGTTT 1440  
TAAAAATATT CAACCATTAT AGGAGGAGAG TTAGTAAAAA GTGAATCTTT CACTTTAGCC 1500  
CCTGACACCT TTCCCCCAA AATATATATT TTGGTGTCTT ATATACAGAA TATACATTCT 1560  
GTGCATATAC AAGAGTATAT GTTGCAGCAT AAAGATTAAA AGCTATTAAA GTTTTTTTTC 1620  
GCTCGTTA 1628

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SPLNFET02
- (B) CLONE: 2203226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125 :

GTGGCGGCGG CGAAGGATGC ACCCGGCAGG CTTGGCGGCG GCGGCTGCGG GGACGCCCCG 60  
GCTGCCCTCG AAGCGGAGGA TCCCTGTGTC CCAGCCGGGC ATGGCCGACC CCCACCAGCT 120  
TTTCGATGAC ACAAGTTCAG CCCAGAGCCG GGGCTATGGG GCCCAGCGGG CACCTGGTGG 180  
CCTGAGTTAT CCTGCAGCCT CTCCCACGCC CCATGCAGCC TTCCTGGCTG ACCCGGTGTC 240  
CAACATGGCC ATGGCCTATG GGAGCAGCCT GGCCGCGCAG GGCAAGGAGC TGGTGGATAA 300  
GAACATCGAC CGCTTCATCC CCATCACCAA GCTCAAGTAT TACTTTGCTG TGGACACCAT 360  
GTATGTGGGC AGAAAGCTGG GCCTGCTGTT CTTCCCCTAC CTACACCAGG ACTGGGAAGT 420  
GCAGTACCAA CAGGACACCC CGGTGGCCCC CCGCTTTGAC GTCAATGCCC CGGACCTCTA 480  
CATTCCAGCA ATGGCTTTCA TCACCTACGT TTTGGTGGCT GGTCTTGCGC TGGGGACCCA 540  
GGATAGGTTT TCCCCAGACC TCCTGGGGCT GCAAGCGAGC TCAGCCCTGG CCTGGCTGAC 600  
CCTGGAGGTG CTGGCCATCC TGCTCAGCCT CTATCTGGTC ACTGTCAACA CCGACCTCAC 660  
CACCATCGAC CTGGTGGCCT TCTTGGGCTA CAAATATGTC GGGATGATTG GCGGGGTCCT 720  
CATGGGCCTG CTCTTCGGA AGATTGGCTA CTACCTGGTG CTGGGCTGGT GCTGCGTGGC 780  
CATCTTTGTG TTCATGATCC GGACGCTGCG GCTGAAGATC TTGGCAGACG CAGCAGCTGA 840  
GGGGGTCCCG GTGCGTGGGG CCCGGAACCA GCTGCGCATG TACCTGACCA TGGCGGTGGC 900  
GGCGGCGCAG CCTATGCTCA TGTACTGGCT CACCTTCCAC CTGGTGCGGT GAGCGCGCCC 960  
GCTGAACCTC CCGCTGCTGC TGCTGCTGCT GGGGGCCACT GTGGCCGCCG AACTCATCTC 1020

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CTGCCTGCAG GCCCAAGGT CCACCCTGTC TGGCCACAGG CACCGCCTCC ATCCCATGTC 1080  
CCGCCCAGCC CCGCCCCCAA CCAAGGTGC TGAGAGATCT CCAGCTGCAC AGGCCACCGC 1140  
CCCAGGGCGT GGCCGCTGTT ACAGAAACAA TAAACCCTGA TGGGCATGGC AAAAAAAAAA 1200

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1093 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT16
- (B) CLONE: 2232884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126 :

AGAGCCCCAG CCACGCCGGC CCAGGTGGCC TCAGGTGAGG GGGGGCGGAC GCACCTGTGG 60  
GGACGGGACG ACGAGTTCAA GCCTCCGTGG GTGCAGTTGG TCGCCAGCGA GGGATGCGGA 120  
GACGCCCCTG AACGACCATG GCATCGGCCG ACGAGCTGAC CTTCCATGAA TTCGAGGAGG 180  
CCACTAATCT TCTGGCTGAC ACCCCAGATG CAGCCACCAC CAGCAGAAGC GATCAGCTGA 240  
CCCCACAAGG GCACGTGGCT GTGGCCGTGG GCTCAGGTGG CAGCTATGGA GCCGAGGATG 300  
AGGTGGAGGA GGAGAGTGAC AAGGCCGCGC TCCTGCAGGA GCAGCAGCAG CAGCAGCAGC 360  
CGGGATTCTG GACCTTCAGC TACTATCAGA GCTTCTTTGA CGTGGACACC TCACAGGTCC 420  
TGGACCGGAT CAAAGGCTCA CTGCTGCCCC GGCCTGGCCA CAACTTTGTG CGGCACCATC 480  
TGCGGAATCG GCCGGATCTG TATGGCCCCC TCTGGATCTG TGCCACGTTG GCCTTTGTCC 540  
TGGCCGTCAC TGGCAACCTG ACGCTGGTGC TGGCCCAGAG GAGGGACCCC TCCATCCACT 600  
ACAGCCCCCA GTTCCACAAG GTGACCGTGG CAGGCATCAG CATCTACTGC TATGCGTGGC 660  
TGGTGCCCCC GGCCCTGTGG GGCTTCCTGC GGTGGCGCAA GGGTGTCCAG GAGCGCATGG 720  
GGCCCTACAC CTTCTGGAG ACTGTGTGCA TCTACGGCTA CTCCCTCTTT GTCTTCATCC 780  
CCATGGTGGT CCTGTGGCTC ATCCCTGTGC CTTGGCTGCA GTGGCTCTTT GGGGCGCTGG 840  
CCCTGGGCCT GTCAGCCGCC GGGCTGGTAT TCACCCCTCTG GCCCGTGGTC CGTGAGGACA 900  
CCAGGCTGGT GGCCACAGTG CTGCTGTCCG TGGTCGTGCT GCTCCACGCC CTCCTGGCCA 960  
TGGGCTGTAA GTTGTACTTC TTCCAGTCGC TGCCTCCGGA GAACGTGGCT CCTCCACCCC 1020  
AAATCACATC TCTGCCCTCA AACATCGCGC TGTCCCCTAC CTTGCCGCAG TCCCTGGCCC 1080  
CCTCCTAGGA AGG 1093

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT11
- (B) CLONE: 2328134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127 :

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GCGGGGGATG ACGCCACGGA CATGGTGGCC GAGACCGGCG GGGTGGGGGA CGTGTCGCGC 60
GGCCGGGTGG CCTCGGTCGG TACCCTGGGC GCGGACAGCT GCCTCATTAG TATTCGTACC 120
CACGAGGCGG CGCAGCGGGC CCTCGGGGAC AGCGAGCGTC GCGGCTATGG CTTATCACTC 180
GGGCTACGGA GCCCACGGCT CCAAGCACAG GGCCCGGGCA GCCCGGATC CCCCTCCCTT 240
CTTCGATGAC ACAAGCGGTG GTTATTCCAG CCAGCCCGGG GGATACCCAG CCACAGGAGC 300
AGACGTGGCC TTCAGTGTCA ACCACTTGCT TGGGGACCCA ATGGCCAATG TGGCTATGGC 360
CTATGGCAGC TCCATCGCAT CCCATGGGAA GGACATGGTG CACAAGGAGC TGCACCGTTT 420
TGTGTCTGTG AGCAAAC TCA AGTATTTTTT TGCTGTGGAC ACAGCCTACG TGGCCAAGAA 480
GCTAGGGCTG CTGGTCTTCC CCTACACACA CCAGAACTGG GAAGTGCAGT ACAGTCGTGA 540
TGCTCCTCTG CCCCCCGGC AAGACCTCAA CGCCCCTGAC CTCTATATCC CCACGATGGC 600
CTTCATTACT TACGTGCTCC TGGCTGGGAT GGCAC TGGGC ATTCAGAAAA GGTTCTCCCC 660
GGAGGTGCTG GGCCTGTGTG CAAGCACAGC GCTGGTGTGG GTGGTGATGG AGGTGCTGGC 720
CCTGCTCCTG GGCCTCTACC TGGCCACCGT GCGCAGTGAC CTGAGCACCT TTCACCTGCT 780
GGCCTACAGT GGCTACAAAT ACGTGGGAAT GATCCTCAGT GTGCTCACGG GGCTGCTGTT 840
CGGCAGCGAT GGCTACTACG TGGCGCTGGC CTGGACCTCA TCGGCGCTCA TGTACTTCAT 900
TGTGCGCTCT TTGCGGACAG CAGCCCTGGG CCCCACAGC ATGGGGGGCC CCGTCCCCCG 960
GCAGCGTCTC CAGCTCTACC TGACTCTGGG AGCTGCAGCC TTCCAGCCCC TCATCATATA 1020
CTGGCTGACT TTCCACCTGG TCCGGTGACC CCCTGGCCCC AGATGGCACT GAGTTTTTCA 1080
TTCATTGAAG ATTTGATTTC CTTGAAAAAA AAAAAAAAAG G 1121

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(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1861 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: ISLTNOT01  
 (B) CLONE: 2382718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128 :

CGCGGACTGT GTCTGTTCCC AGGAGTCCTT CGGCGGCTGT TGTGTCAGTG GCCTGATCGC 60  
 GATGGGGACA AAGGCGCAAG TCGAGAGGAA ACTGTTGTGC CTCTTCATAT TGGCGATCCT 120  
 GTTGTGCTCC CTGGCATTGG GCAGTGTTAC AGTGCACTCT TCTGAACCTG AAGTCAGAAT 180  
 TCCTGAGAAT AATCCTGTGA AGTTGTCCTG TGCCTACTCG GGCTTTTCTT CTCCCCGTGT 240  
 GGAGTGGAAG TTTGACCAAG GAGACACCAC CAGACTCGTT TGCTATAATA ACAAGATCAC 300  
 AGCTTCCTAT GAGGACCGGG TGACCTTCTT GCCAACTGGT ATCACCTTCA AGTCCGTGAC 360  
 ACGGGAAGAC ACTGGGACAT ACACTTGTAT GGTCTCTGAG GAAGGCGGCA ACAGCTATGG 420  
 GGAGGTCAAG GTCAAGCTCA TCGTGCTTGT GCCTCCATCC AAGCCTACAG TTAACATCCC 480  
 CTCCTCTGCC ACCATTGGGA ACCGGGCAGT GCTGACATGC TCAGAACAAG ATGGTTCCCC 540  
 ACCTTCTGAA TACACCTGGT TCAAAGATGG GATAGTGATG CCTACGAATC CAAAAGCAC 600  
 CCGTGCCTTC AGCAACTCTT CCTATGTCCT GAATCCCACA ACAGGAGAGC TGGTCTTTGA 660  
 TCCCCTGTCA GCCTCTGATA CTGGAGAATA CAGCTGTGAG GCACGGAATG GGTATGGGAC 720  
 ACCCATGACT TCAAATGCTG TGCGCATGGA AGCTGTGGAG CGGAATGTGG GGGTCATCGT 780  
 GGCAGCCGTC CTTGTAACCC TGATTCTCCT GGAATCTTG GTTTTTGGCA TCTGGTTTGC 840  
 CTATAGCCGA GGCCACTTTG ACAGAACAAA GAAAGGGACT TCGAGTAAGA AGGTGATTTA 900  
 CAGCCAGCCT AGTGCCCGAA GTGAAGGAGA ATTCAAACAG ACCTCGTCAT TCCTGGTGTG 960  
 AGCCTGGTCG GCTCACCGCC TATCATCTGC ATTTGCCTTA CTCAGGTGCT ACCGGACTCT 1020  
 GGCCCTGAT GTCTGTAGTT TCACAGGATG CCTTATTTGT CTTCTACACC CCACAGGGCC 1080  
 CCCTACTTCT TCGGATGTGT TTTTAATAAT GTCAGCTATG TGCCCCATCC TCCTTCATGC 1140  
 CCTCCCTCCC TTTCTACCA CTGCTGAGTG GCCTGGAACT TGTTTAAAGT GTTTATTCCC 1200  
 CATTTCTTTG AGGGATCAGG AAGGAATCCT GGGTATGCCA TTGACTTCCC TTCTAAGTAG 1260  
 ACAGCAAAAA TGGCGGGGGT CGCAGGAATC TGCACTCAAC TGCCACCTG GCTGGCAGGG 1320  
 ATCTTTGAAT AGGTATCTTG AGCTTGGTTC TGGGCTCTTT CTTGTGTAC TGACGACCAG 1380  
 GGCCAGCTGT TCTAGAGCGG GAATTAGAGG CTAGAGCGGC TGAAATGGTT GTTTGGTGAT 1440  
 GAACTGGGG TCCTTCCATC TCTGGGGCCC ACTCTCTTCT GTCTTCCCAT GGAAGTGCC 1500

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ACTGGGATCC CTCTGCCCTG TCCTCCTGAA TACAAGCTGA CTGACATTGA CTGTGTCTGT 1560  
GGAAAATGGG AGCTCTTGTT GTGGAGAGCA TAGTAAATTT TCAGAGAACT TGAAGCCAAA 1620  
AGGATTTAAA ACCGCTGCTC TAAAGAAAAG AAAACTGGAG GCTGGGCGCA GTGGCTCACG 1680  
CCTATAATCC CAGAGGCTGA GGCAGGCGGA TCACCTGAGG TCGGGAGTTC GGGATCAGCC 1740  
TGACCAACAT GGAGAAACCC TACTGAGAAT ACAAAGTTAG CCAGGCATGG TGGTGCATGC 1800  
CTGTAATCCC AGCTGCTCAG GAGCCTGGCA ACAAGAGCAA AACTCCAGCT CAAAAAAAAA 1860  
A 1861

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ENDANOT01
- (B) CLONE: 2452208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129 :

GTTTGGAGGA GACTCGGATA TACCTTCTCA GAAGCTGCAC AGGAGGAAAG CAGTGACAAA 60  
GAAAGAAGTT GTCATTCTTT GCACGAAACT GGATGGCTTC TACAGGGAGC CAGGCCTCTG 120  
ATATAGACGA GATTTTTTGA TTCTTCAACG ATGGCGAACC TCCCACCAA AAGCCCAGGA 180  
AGCTGCTTCC AAGCTTAAAA ACTAAGAAGC CTCGAGAACT TGTGCTAGTG ATTGGAACAG 240  
GCATTAGTGC TGCAGTTGCG CCCCAAGTTC CAGCCCTCAA ATCCTGGAAG GGGTTAATTC 300  
AGGCCTTACT GGATGCTGCC ATTGATTTTG ATCTTTTAGA AGATGAGGAG AGCAAAAAGT 360  
TTCAGAAATG TCTCCATGAA GACAAGAACC TGGTCCATGT TGCCCATGAC CTTATCCAGA 420  
AACTCTCTCC TCGTACCAGT AATGTTTCGAT CCACATTTTT CAAGGACTGT TTATATGAAG 480  
TATTTGATGA CTTGGAGTCA AAGATGGAAG ATTCTGGAAA ACAGCTACTT CAGTCAGTTC 540  
TCCACCTGAT GGAAAATGGA GCCCTCGTAT TAACTACAAA TTTTGATAAT CTCTTGGAAC 600  
TGTATGCAGC AGATCAGGGG AAACAGCTTG AATCCCTTGA CTTACTGAT GAGAAAAAGG 660  
TCCTCGAGTG GGCTCAGGAG AAGCGTAAGC TGAGCGTGTT GCATATTCAC GGAGTCTACA 720  
CCAACCCTAG TGGCATTGTC CTTCATCCGG CTGGATATCA GAACGTGCTC AGGAACACTG 780  
AAGTCATGAG AGAAATTGAG AAACCTCTACG AAAACAAGTC ATTTCTTTTC CTGGGCTGTG 840  
GCTGGACTGT GGATGACACC ACTTTCCAGG CCCTTTTCTT GGAGGCTGTC AAGCATAAAT 900



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CTGACCTAGA ACATTTTCATG CTGGTTTCGGA GAGGAGACGT AGATGAGTTC AAAAAGCTTC 960  
GAGAAAACAT GCTGGACAAG GGGATTAAAG TCATCTCCTA TGGAGATGAC TATGCCGATC 1020  
TTCCAGAATA TTTCAAGCGA CTGACATGTG AGATCTCCAC AAGGGGTACA TCAGCAGGGA 1080  
TGGTGAGAGA AGGTCAGCTA AATGGCTCAT CTGCAGCACA CAGTGAAATA AGAGGCTGTA 1140  
GTACATGAGC GAGCTAGAGA AATCACCACC GTTTAGACCA AGCTGTAAGG CCCTACTACA 1200  
GACAGTGTTT AACAAAGTAA CTTACAAGAA CCCAACACAA TTCCCAGAAA GTAACAATAG 1260  
CCAGAGGTTG AAGGGCGGGG TAGAAGAGGG GGAATGTTG CAGCGTAATC CTTCATACCA 1320  
CCTGGTTCTT GATATTCTGC CGCCTGTTCA AGTTCAAGAA TAAAAGCGAC AGCAGGACCC 1380  
AAATGCAGCT CCCAACCCAC TCCCCAGGCT AGACATGCTT GTGTCCACAC AGCACACCAA 1440  
TGTGATACTT CCACTGACCG GCTGCAGCTC TGCATGAAGG ACTCGGGGTC TGGATGCCAT 1500  
GGAATCACTG TGGCTCTTGT TGCAGTTTTG TACTCTATAC TTGGTTTTTC AATTAAGCTT 1560  
AATGGCTTTT TTTAAACATG ACTTGAAGCT CTAGTTTTCT AGATCTTTTA CAGTGTACAG 1620  
TATTTTACAT AACTAAGCTG TATTAAAAGC TTGTTCAATTT ACTTGCCAGG ACCCTGGCTC 1680  
TACTTTTAGA GTCATTGTAA GAAACTCTAA CTTGCATCAA GGTACTAATA AGCTTAATTT 1740  
TAATAACCCA AAGTTTAAAG GTTCCGATCT TTCTCCTTGG GGTGGAGTGA TCTCATTCTC 1800  
AGGACAACCG TTTACTTACC TGATTCCTCG GAGCATTATC AACTTCTGCT CTGTTGTCCT 1860  
GACCATACAT ATGTCCTAGA ACTACAGTTA AGTGTGTTGT GGAATTTTAG TTTTGAATCC 1920  
GGAATAAATG AAGTCCCAGG ACTCAAAGAA GAGAGAAAAA AAAAAAGGGG GCCCC. 1975

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ENDANOT01
- (B) CLONE: 2457825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130 :

TCTACTGTCC CCTGCCCTGT ACCCCCAGGC ATTGATCTGG AGAACATTGT GTECTACAAG 60  
GACGACACCC ACTACTTTGT GATGACAGCC AAGAAGCAGT GCCTGCTGCG GCTGGGGGTG 120  
CTGCGCCAGG ACTGGCCAGA CACCAATCGG CTGCTGGGCA GTGCCAATGT GGTGCCCCGAG 180  
GCTCTGCAGC GCTTTACCCG GGCAGCTGCT GACTTTGCCA CCCATGGCAA GCTCGGGAAA 240

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CTAGAGTTTG CCCAGGATGC CCATGGGCAG CCTGATGTCT CTGCCTTTGA CTTACGAGC 300  
ATGATGCGGG CAGAGAGTTC TGCTCGTGTG CAAGAGAAGC ATGGCGCCCG CCTGCTGCTG 360  
GGACTGGTGG GGGACTGCCT GGTGGAGCCC TTCTGGCCCC TGGGCACTGG AGTGGCACGG 420  
GGCTTCCTGG CAGCCTTTGA TGCAGCCTGG ATGGTGAAGC GGTGGGCAGA GGGCGCTGAG 480  
TCCCTAGAGG TGTTGGCTGA GCGTGAGAGC CTGTACCAGC TTCTGTCACA GACATCCCCA 540  
GAAAACATGC ATCGCAATGT GGCCAGTAT GGGCTGGACC CAGCCACCCG CTACCCCAAC 600  
CTGAACCTCC GGGCAGTGAC CCCCAATCAG GTACGAGACC TGTATGATGT GCTAGCCAAG 660  
GAGCCTGTGC AGAGGGACAA CGACAAGACA GATACAGGGA TGCCAGCCAC CGGGTCGGCA 720  
GGCACCCAGG AGGAGCTGCT ACGCTGGTGC CAGGAGCAGA CAGCTGGGTA CCCGGGAGTC 780  
CACGTCTCCG ATTTGTCTTC CTCCTGGGCT GATGGGCTAG CTCTGTGTGC CCTGGTGTAC 840  
CGGCTGCAGC CTGGCCTGCT GGAACCCCTCA GAGCTGCAGG GGCTGGGAGC TCTGGAAGCA 900  
ACTGCTTGGG CACTAAAGGT GGCAGAGAAT GAGCTGGGCA TCACACCGGT GGTGTCTGCA 960  
CAGGCCGTGG TAGCAGGGAG TGACCCACTG GGCCTCATTG CCTACCTCAG CCACTTCCAC 1020  
AGTGCCTTCA AGAGCATGGC CCACAGCCCA GGCCCTGTCA GCCAGGCCTC CCCAGGGACC 1080  
TCCAGTGCTG TATTATTCCT TAGTAAACTT CAGAGGACCC TGCAGCGATC CCGGGCCAAG 1140  
GAAAATGCAG AGGATGCTGG TGGCAAGAAG CTGCGCTTGG AGATGGAGGC CGAGACCCCA 1200  
AGTACTGAGG TGCCACCTGA CCCAGAGCCT GGTGTACCCC TGACACCCCA ATCCCAACAC 1260  
CAGGAGGCCG GTGCTGGGGA CCTGTGTGCA CTTTGTGGGG AACACCTCTA TGTCTGGAA 1320  
CGCCTCTGTG TCAACGGCCA TTTCTTCCAC CGGAGCTGCT TCCGCTGCCA TACCTGTGAG 1380  
GCCACACTGT GGCCAGGTGG CTACGAGCAG CACCCAGGCA GTAGAACGTC TCAGTTCTTC 1440  
TTCTCAGCTC TTGTGGCCAT GGAGAAGGAG GAAAAAGAGA GTCCCTTCTC CAGTGAAGAG 1500  
GAAGAAGAAG ATGTGCCTTT GGA CTAGAT GTGGAACAGG CCCTGCAGAC CTTTGCCAAG 1560  
ACCTCAGGCA CCATGAATAA CTACCCAACA TGGCGTCGGA CTCTGCTGCG CCGTGCGAAG 1620  
GAGGAGGAGA TGAAGAGGTT CTGCAAGGCC CAGACCATCC AACGGCGACT AAATGAGATT 1680  
GAGGCTGCCT TGAGGGAGCT AGAGGCCGAG GGC GTGAAGC TGGAGCTGGC CTTGAGGCGC 1740  
CAGAGCAGTT CCCCAGAACA GCAAAAGAAA CTATGGGTAG GACAGCTGCT ACAGCTCGTT 1800  
GACAAGAAAA ACAGCCTGGT GGCTGAGGAG GCCGAGCTCA TGATCACGGT GCAGGAATTG 1860  
AATCTGGAGG AGAAACAGTG GCAGCTGGAC CAGGAGCTAC GAGGCTACAT GAACCGGGAA 1920  
GAAAACCTAA AGACAGCTGC TGATCGGCAG GCTGAGGACC AGGTCCTGAG GAAGCTGGTG 1980  
GATTTGGTCA ACCAGAGAGA TGCCCTCATC CGCTTCCAGG AGGAGCGCAG GCTCAGCGAG 2040  
CTGGCCTTGG GGACAGGGGC CCAGGGCTAG ACGAGGGTGG GCCGTCTGCT TTCGTTCCCA 2100

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CAAAGAAAGC ACCTCACCCC AGCACAGTGC CACCCCTGTT CATCTGGGCT GCCTGGCAGA 2160

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1NOT03
- (B) CLONE: 2470740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131 :

GAGGAAGAAG AGGAAGAGGG GGCTCCGATT GGGACCCCTA GGGATCCTGG AGATGGTTGT 60  
CCTTCCCCCG ACATCCCTCC TGAACCCCT CCAACACACC TGAGGCCCTG CCCTGCCAGC 120  
CAGCTCCCTG GACTCCTGTC CCATGGCCTC CTGGCCGGCC TCTCCTTTGC AGTGGGGTCC 180  
TCCTCTGGCC TCCTGCCCCT CCTGCTGCTG CTGCTGCTTC CATTGCTGGC AGCCCAGGGT 240  
GGGGGTGGCC TGCAGGCAGC GCTGCTGGCC CTTGAGGTGG GGCTGGTGGG TCTGGGGGCC 300  
TCCTACCTGC TCCTTTGTAC AGCCCTGCAC CTGCCCTCCA GTCTTTTCCT ACTCCTGGCC 360  
CAGGGTACCG CACTGGGGGC CGTCCTGGGN CATGAGCTGG CGCCGAAGGC TCATGGGTGT 420  
TCCCCTGGGG CTTTGGAACT GCCTGGTTCT TAAGCTTNGG CAAGGCCTAG CTCCAACCTC 480  
TGGTGGCTAA TGGCANCCGG GGGGGAANAT GGGTTCNGGA AAAAGGGCCC CCGGGTTTCA 540  
CCGGGG 546

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SMCANOT01
- (B) CLONE: 2479092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132 :

GCCATGGAGG CCCTGAGGAG GGCCACGAG GTCGCGCTCC GCCTGCTGCT GTGTAGGCCG 60  
TGGGCCTCGC GCGCCGCCGC CCGCCCCAAG CCCAGCGCCT CGGAGGTGCT GACGCGGCAT 120

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CTGCTGCAGC GGCGCCTGCC GCACTGGACC TCCTTCTGCG TGCCCTACAG CGCCGTCCGC 180  
AACGACCAGT TCGGCCTCTC GCACTTCAAC TGGCCGGTGC AGGGCGCCAA CTACCACGTC 240  
CTGCGCACCG GCTGCTTCCC CTTTCATCAAG TACCACTGCT CCAAGGCTCC CTGGCAGGAC 300  
CTGGCCCGGC AGAACCGCTT CTTACGGCG CTCAAGGTCG TCAACCTCGG TATTCCAAC 360  
TTATTATATG GACTTGGCTC CTGGTTATTT GCCAGAGTCA CAGAGACTGT GCATACCAGT 420  
TATGGACCCA TAACAGTTTA TTTTCTCAAT AAAGAAGATG AAGGTGCCAT GTATTGAAAG 480  
TGTGCGTCAA AGAACATAAA TATCAGTGGA TTTTCTCTGT GTATATGTGC AGTATTTATT 540  
TTTGATCCTT TAAAATAAAA CTTTTGCAAA TAAAAA A 581

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SMCANOT01
- (B) CLONE: 2480544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133 :

GGGCTGGGCC CCGCCGAGC TCCAGCTGGC CGGCTTGGTC CTGCGGTCCC TTCTCTGGGA 60  
GGCCCGACCC CGGCCGCGCC CAGCCCCAC CATGCCACCC GCGGGGCTCC GCCGGGCCGC 120  
GCCGCTCACC GCAATCGCTC TGTTGGTGCT GGGGGCTCCC CTGGTGCTGG CCGGCGAGGA 180  
CTGCCTGTGG TACCTGGACC GGAATGGCTC CTGGCATCCG GGGTTTAACT GCGAGTTCTT 240  
CACCTTCTGC TGCGGGACCT GCTACCATCG GTACTGCTGC AGGGACCTGA CCTTGCTTAT 300  
CACCGAGAGG CAGCAGAAGC ACTGCCTGGC CTTAGCCCC AAGACCATAG CAGGCATCGC 360  
CTCAGCTGTG ATCCTCTTTG TTGCTGTGGT TGCCACCACC ATCTGCTGCT TCCTCTGTTC 420  
CTGTTGCTAC CTGTACCGCC GGCGCCAGCA GCTCCAGAGC CCATTTGAAG GCCAGGAGAT 480  
TCCAATGACA GGCATCCCAG TGCAGCCAGT ATACCCATAC CCCCAGGACC CCAAAGCTGG 540  
CCCTGCACCC CCACAGCCTG GCTTCATGTA CCCACCTAGT GGTCTGCTC CCCAATATCC 600  
ACTCTACCCA GCTGGGCCCC CAGTCTACAA CCCTGCAGCT CCTCCTCCCT ATATGCCACC 660  
ACAGCCCTCT TACCCGGGAG CCTGAGGAAC CAGCCATGTC TCTGCTGCCC CTTAGTGAT 720  
GCCAACCTTG GGAGATGCCC TCATCCTGTA CCTGCATCTG GTCCTGGGGG TGGCAGGAGT 780  
CCTCCAGCCA CCAGGCCCCA GACCAAGCCA AGCCCTGGGC CCTACTGGGG ACAGAGCCCC 840

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AGGGAAGTGG AACAGGAGCT GAACTAGAAC TATGAGGGGT TGGGGGGAGG GCTTGAATT 900  
ATGGGCTATT TTTACTGGGG GCAAGGGAGG GAGATGACAG CCTGGGTCAC AGTGCCTGTT 960  
TTCAAATAGT CCCTCTGCTC CCAAGATCCC AGCCAGGAAG GCTGGGGCCC TACTGTTTGT 1020  
CCCCTCTGGG CTGGGGTGGG GGGAGGGAGG AGGTTCCGTC AGCAGCTGGC AGTAGCCCTC 1080  
CTCTCTGGCT GCCCCACTGG CCACATCTCT GGCCTGCTAG ATTAAAGCTG TAAAGACATA 1140  
ACTCATATCA GTCGCATCAT TGGACCCATC CACACCTTCC AGGAACACCG NCTTCAGCTG 1200  
GGCCCAGACT GTTGCCCACT CCATATTCCA AAAGTAGGGG AGGGCCAGCA CCAGCATCG 1259

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2033 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT21
- (B) CLONE: 2518547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134 :

CGGCTCGAGG CCGCAGCCCC ATGGACAGTC TTCTGCACCC CCGGGAGCGC CCTGGATCCA 60  
CTGCCTCCGA GAGCTCAGCC TCTCTGGGCA GTGAGTGGA CCTCTCAGAA TCTTCTCTCA 120  
GCAACCTGAG TCTTCGCCGT TCCTCAGAGC GCCTCAGTGA CCCCCCTGGA TCCTTCCAGT 180  
CACCTTCCCT GGAAATTCTG CTGTCCAGCT GCTCCCTGTG CCGTGCCTGT GATTGCTGG 240  
TGTATGATGA GGAAATCATG GCTGGCTGGG CACCTGATGA CTCTAACCTC AACACAACCT 300  
GCCCCCTCTG CGCCTGCCCC TTTGTGCCCC TGCTCAGTGT CCAGACCCTT GATTCCCGGC 360  
CCAGTGTCCT CAGCCCCAAA TCTGCTGGTG CCAGTGGCAG CAAAGATGCT CCTGTCCCTG 420  
GTGGTCCTGG CCCTGTGCTC AGTGACCGAA GGCTCTGCCT TGCTCTGGAT GAGCCCAGCT 480  
CTGCAACGGG CACATGGGGG GAGCCTCCCG GCGGGTTGAG AGTGGGGCAT GGGCATACT 540  
GAGCCCCCTG GTGCTGCGTA AGGAGCTGGA GTCGCTGGTA GAGAACGAGG GCAGTGAGGT 600  
GCTGGCGTTG CCTGAACTGC CCTCTGCCCA CCCCATCATC TTCTGGAACC TTTTGTGGTA 660  
TTTCCAACGG CTACGCCTGC CCAGTATTCT ACCAGGCCTG GTGCTGGCCT CCTGTGATGG 720  
GCCTTCGCAC TCCCAGGCCC CATCTCCTTG GCTAACCCTT GATCCAGCCT CTGTTCAGGT 780  
ACGGCTGCTG TGGGATGTAC TGACCCCTGA CCCCAATAGC TGCCCACCTC TCTATGTGCT 840  
CTGGAGGGTC CACAGCCAGA TCCCCAGCG GGTGGTATGG CCAGGCCCTG TACCTGCATC 900

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CCTTAGTTTG GCACTGTTGG AGTCAGTGCT GCGCCATGTT GGACTCAATG AAGTGCACAA 960  
GGCTGTGGGG CTCCTGCTGG AAACCTCTAGG GCCCCACCC ACTGGCCTGC ACCTGCAGAG 1020  
GGGAATCTAC CGTGAGATAT TATTCCTGAC AATGGCTGCT CTGGGCAAGG ACCACGTGGA 1080  
CATAGTGGCC TTCGATAAGA AGTACAAGTC TGCCTTTAAC AAGCTGGCCA GCAGCATGGG 1140  
CAAGGAGGAG CTGAGGCACC GCGGGGCGCA GATGCCCACT CCAAGGCCA TTGACTGCCG 1200  
AAAAATGTTTT GGAGCACCTC CAGAATGCTA GAGACCTTAA GCTTCCCTCT CCAGCCTAGG 1260  
GTGGGGAAGT GAGGAAGAAG GGATTCTAGA GTTAACTGC CTCCCTGTTG CCTTCATGGA 1320  
GTTGGGAACA GGCTGGGAAG GATGCCCAGT CAAAGGCTCC AAGCGAGGAC AACAGGAAGA 1380  
GGGATCCACT GTTACCAAAA GTCCTGATTC CCCCATCACC AACCTACCCA GTTTGTTCTG 1440  
GCTGATGTTG GGGGAGATCT GGGGGGAGTT GGTACAGCTC TGTTCCTCCC TTGTCCTATA 1500  
CCGGGAACTC CCCTCCAGGG TACCCACAGA TCTGCATTGC CCTGGTCATT TTAGAAGTTT 1560  
TTGTTTTTAA AAACAACCTG AAAGATGCAG AGCTACTGAG CCTTTGCCCT GAATGGGAGG 1620  
TAGGGATGTC ATTCTCCACC AATAATGGTC CCTCTTCCCT GACGTTGCTG AAGGAGCCCA 1680  
AGGCTCTCCA TGCCTTTCTA CCTAAGTGTT TGTATTTTAT TTTAAATTAT TTATTCTGGA 1740  
GCCACAGCCC CCTTGCTTAT GAGGTTCTTA TGGAGAGTGA GAAAGGGAAG GGAAATAGGG 1800  
CACCATGGTC CGGTGGTTTG TAGTTCCTTC AAAGTCAGGC ACTGGGAGCT AGAGGAGTCT 1860  
CAAGCTCCCC TTAGGAAGAA CTGGTGCCCC CTCCAGTCCT AATTTTCTT GCCTGCCCCG 1920  
CCTTGGGGAA TGCCTCACCC ACCCAGGTCC TGACCTGTGC AATAAGGATT GTTCCCTGCG 1980  
AAGTTTTGTT GGATGTAAAT ATAGTAAAAG CTGCTTCTGT CTTTTTCAAA AAA 2033

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GBLANOT02
- (B) CLONE: 2530650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135 :

GCCCACTGGG CTCTCCCGGC TGCAGTGCCA GGGCGCAGGA CGCGGCCGAT CTCCCGCTCC 60  
CGCCACCTCC GCCACCATGC TGCTCCCCCA GCTCTGCTGG CTGCCGCTGC TCGCTGGGCT 120  
GCTCCCGCCG GTGCCCCTC AGAAGTTCTC GCGCTCACG TTTTGTGAGAG TGGATCAAGA 180

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TAAAGACAAG GATTGTAGCT TGGACTGTGC GGGTTCGCCC CAGAAACCTC TCTGCGCATC 240  
TGACGGAAGG ACCTTCCTTT CCCGTTGTGA ATTTCAACGT GCCAAGTGCA AAGATCCCCA 300  
GCTAGAGATT GCATATCGAG GAAACTGCAA AGACGTGTCC AGGTGTGTGG CCGAAAGGAA 360  
GTATACCCAG GAGCAAGCCC GGAAGGAGTT TCAGCAAGTG TTCATTCTTG AGTGCAATGA 420  
CGACGGCACC TACAGTCAGG TCCAGTGTCA CAGCTACACG GGATACTGCT GGTGCGTCAC 480  
GCCCCACGGG AGGCCCATCA GCGGCACTGC CGTGGCCCCAC AAGACGCCCC GGTGCCCCGG 540  
TTCCGTAAAT GAAAAGTTAC CCCAACGCGA AGGCACAGGA AAAACAGATG ATGCCGCAGC 600  
TCCAGCGTTG GAGACTCAGC CTCAAGGAGA TGAAGAAGAT ATTGCATCAC GTTACCCTAC 660  
CCTTTGGACT GAACAGGTTA AAAGTCGGCA GAACAAAACC AATAAGAATT CAGTGTTCATC 720  
CTGTGACCAA GAGCACCAGT CTGCCCTGGA GGAAGCCAAG CAGCCCAAGA ACGACAATGT 780  
GGTGATCCCT GAGTGTGCGC ACGGCGGCCT CTACAAGCCA GTGCAGTGCC ACCCCTCCAC 840  
GGGGTACTGC TGGTGCCTCC TGGTGGACAC GGGGCGCCCC ATTCCCGGCA CATCCACAAG 900  
GTACGAGCAG CCGAAATGTG ACAACACGGG CCAGGGCCCCA CCCAGCCAAA GCCCGGGACC 960  
TGTACAAGGG CCGCCAGCTA CAAGGTTGTC CGGGTGCCAA AAAGCATGAG TTTCTGACCA 1020  
GCGTTCTGGA CGCGCTGTCC ACGGACATGG TCCACGCCGC CTCCGACCCC TCCTCCTCGT 1080  
CAGGCAGGCT CTCAGAACCC GACCCAGCC ATACCCTAGA GGAGCGGGTG GTGCACTGGT 1140  
ACTTCAAAC ACTGGATAAA AACTCCAGTG GAGACATCGG CAAAAGGAA ATCAAACCTT 1200  
TCAAGAGGTT CCTTCGCAA AAATCAAAGC CCAAAAAATG TGTGAAGAAG TTTGTTGAAT 1260  
ACTGTGACGT GAATAATGAC AAATCCATCT CCGTACAAGA ACTGATGGGC TGCCTGGGCG 1320  
TGGCGAAAGA GGACGGCAA GCGGACACCA AGAAACGCCA CACCCCAAGA GGTCATGCTG 1380  
AAAGTACGTC TAATAGACAG CCAAGGAAAC AAGGATAAAT GGCTCATACC CCGAAGGCAG 1440  
TTCCTAGACA CATGGGAAAT TTCCCTCACC AAAGAGCAAT TAAGAAAACA AAAACAGAAA 1500  
CACATAGTAT TTGCACTTTG TACTTTAAAT GTAAATTCAC TTTGTAGAAA TGAGCTATTT 1560  
AAACAGACTG TTTTAATCTG TGAAAATGGA GAGCTGGCTT CAGAAAATTA ATCACATACA 1620  
ATGTATGTGT CCTCTTTTGA CCTTGGAAT CTGTATGTGG TGGAGAAGTA TTTGAATGCA 1680  
TTTAGGCTTA ATTTCTTCGC CTTCCACATG TTAACAGTAG AGCTCTATGC ACTCCGGCTG 1740  
CAATCGTATG GCTTTCTCTA ACCCCTGCAG TCACTTCCAG ATGCCTGTGC TTACAGCATT 1800  
GTGGAATCAT GTTGAAGCT CCACATGTCC ATGGAAGTTT GTGATGTACG GCCGACCCTA 1860  
CAGGCAGTTA ACATGCATGG GCTGGTTTGT TTCTTGGGAT TTTCTGTTAG TTTGTCTTGT 1920  
TTTGCTTTCC AGAGATCTTG CTCATACAAT GAATCACGCA ACCACTAAAG CTATCCAGTT 1980  
AAGTGCAGGT AGTTCCTCTG GAGGAAATAA TATTTTCAA CTGTCGTTGG TGTGATACTT 2040

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GGGCTCAAAG GATCTTTGCT TTTCCATTTT AAGCTTCTGT TTTGAGTTTT GCCCTGGGGC 2100  
TTGAATGAGT CCCAGAGAGT CGTTCGGATG GTGGGAGGCT GCCTAGGAGG CAGTAAATCC 2160  
AGTCACAGTG CCTGGGAGGG GCCCATCCTT CCAAAATGTA AATCCAGTCG CGGTGTGACC 2220  
GAGCTGGCTA ACAGGCTTGT CTGCCTGGTT TTCCTCCTAC ACGTGGACAT TATTCTCCTG 2280  
ATCCTCCTAC CTGGTCCACC CCAGGGCTAC CGGAAGGTAA AATCTTCACC TGAACCAATT 2340  
ATGAGCAGTC TCCTTACTGA AGGTACAGCC GGATACGTGG TGCCCCCGGG GCTGGTGTG 2400  
GCAGCCGGGG GGAGGTGCCT GAGGGTCCCC ACGGTTCCCTT TCTGCTTTTC TGAATGCATC 2460  
AAGGGTACGA GAACTTGCCA ATGGGAAATT CATCCGAGTG GCACTGGCAG AGAAGGATAG 2520  
GAGTGGAATG CCCACACAGT GACCAACAGA ACTGGTCTGC GTGCATAACC AGCTGCCACC 2580  
CTCAGGCCTG GGCCCCAGAG CTCAGGGCAC CCAGTGTCTT AAGGAACCAT TTGGAGGACA 2640  
GTCTGAGAGC AGGAACTTCA AGCTGTGATT CTATCTCGGC TCAGACTTTT GGTTGGAAAA 2700  
AGATCTTCAT GGCCCCAAT CCCCTGAGAC ATGCCTTGTA GAATGATTTT GTGATGTTGT 2760  
GATGCTTGTG GAGCATCGCG TAAGGCTTCT TGCTTATTTA AACTGTGCAA GGTA AAAATC 2820  
AAGCCTTTGG AGCCACAGAA CCAGCTCAAG TACATGCCAA TGTGTGTTAA GAAACAGTTA 2880  
TGATCCTAAA CTTTTTGGAT AATCTTTTAT ATTTCTGACC TTTGAATTTA ATCATTGTTT 2940  
TTAGATTAAA ATAAATATG CTATTGAAAC TAAAAA AAAAAGAGGGA GAAGAAAAAA 3000  
AAAAAGG 3007

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THYMNOT04
- (B) CLONE: 2652271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136 :

CTCTCTGCTC CGGTGCAGGC CCGCAGGCGC CCTGGGCTGG GAGCAACGCG ACTGACCGTG 60  
GTCGTGGGCG GACGGCGGCT GCAGCGTGGA GGAGCTGGGG TCGCTGTGGG TCGCGAACAG 120  
AGCCCGGGAC GTGCGCGCTT GGTGCACGAT CCTGAAGGGG AGCTCCGAGG GGCCCGGGTC 180  
TCCAGGGCTG CTGCGGCCAT TCCCGGAGCC CGGCGCGGGG CCCGCGAGAT ACTGGTTTAG 240  
GCCGTCCCAG GGCTCCGGGC GCACCCGGTG GCCGCTGCTG CAGCGGAGGG AGCGCGGCGG 300



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CGCGGGGGCT CGGAGACAGC GTTCTCTCCG GAAGTCTTCC TCGGGCAGCA GGTGGGAAGT 360  
GGGAGCCGGA GCGGCAGCTG GCAGCGTTCT CTCCGCAGGT CGGCACCATG CGCCCTGCAG 420  
CCCTGCGCGG GGCCCTGCTG GGCTGCCTCT GCCTGGCGTT GCTTTGCCTG GGCGGTGCGG 480  
ACAAGCGCCT GCGTGACAAC CATGAGTGGA AAAAATAAT TATGGTTCAG CACTGGCCTG 540  
AGACAGTATG CGAGAAAATT CAAAACGACT GTAGAGACCC TCCGATTAC TGGACAATAC 600  
ATGGACTATG GCCCCATAAA AGTGAAGGAT GTAATAGATC GTGGCCCTTC AATTTAGAAG 660  
AGATTAAGGA TCTTTTGCCA GAAATGAGGG CATACTGGCC TGACGTAATT CACTCGTTTC 720  
CCAATCGCAG CCGCTTCTGG AAGCATGAGT GGGAAAAGCA TGGGACCTGC GCCGCCAGG 780  
TGGATGCGCT CAACTCCCAG AAGAAGTACT TTGGCAGAAG CCTGGAAGTC TACAGGGAGC 840  
TGGACCTCAA CAGTGTGCTT CTAAAATTGG GGATAAAACC ATCCATCAAT TACTACCAAG 900  
TTGCAGATTT TAAAGATGCC CTTGCCAGAG TATATGGAGT GATACCCAAA ATCCAGTGCC 960  
TTCCACCAAG CCAGGATGAG GAAGTACAGA CAATTGGTCA GATAGAACTG TGCCTCACTA 1020  
AGCAAGACCA GCAGCTGCAA AACTGCACCG AGCCGGGGGA GCAGCCGTCC CCCAAGCAGG 1080  
AAGTCTGGCT GGCAAATGGG GCCGCCGAGA GCCGGGGTCT GAGAGTCTGT GAAGATGGCC 1140  
CAGTCTTCTA TCCCCACCT AAAAAGACCA AGCATTGATG CCCAAGTTT GGAAATATTC 1200  
TGTTTTAAAA AGCATGAGGT AGGCATGTC 1229

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT11
- (B) CLONE: 2746976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137 :

ACAGGGGCTT CCCCTTCGCC GCCGCCGCCG CCGCCGGCCA AGCTCCGCCG CGCCGCGGC 60  
CCGCGGCCGC CATGCAGTTT ATGTTGCTTT TTAGTCGTCA GGGAAAGCTT CGACTGCAAA 120  
AATGGTATGT CCCACTATCA GACAAAGAGA AGAGAAAGAT CACAAGAGAA CTTGTTTCTA 180  
CCGTTTTAGC ACGGAAACCT AAAATGTGCA GCTTCCTTGA GTGGCGAGAT CTGAAGATTG 240  
TTTACAAAAG ATATGCTAGT CTGTATTTTT GCTGTGCTAT TGAGGATCAG GACAATGAAC 300  
TAATTACCCT GGAAATAATT CATCGTTATG TGAATTACT TGACAAGTAT TTCGGCAGTG 360

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TCTGTGAACT AGATATCATC TTTAATTTTG AGAAGGCTTA TTTTATTTTG GATGAGTTTC 420  
TTTTGGGAGG GGAAGTTCAG GAAACATCCA AGAAAAATGT CCTTAAAGCA ATTGAGCAGG 480  
CTGATCTACT GCAGGAGGAT GCGAAAGAAG CTGAAACCCC ACGTAGTGTT CTTGAAGAAA 540  
TTGGACTGAC ATAACTCTCC TCCCTTGTTG ATGACTTCTT GTGGCATTTC ACACACTGTA 600  
GATGGTCACT CCCTTCATGT CCATGTTAGC TCATGGTGTA AGATGATGTC TTGTCAGTAT 660  
TACTGTTTTG CTAAGCCGCT TCATTCATGC CTACACAATT TTTTTTTAAA AGGGAACTTT 720  
AGTTAATTAA GTGATAAGGG ACTTAAATAT GAATTAGAAT GGTGCAGAAA GAGATACCTT 780  
TTCTGGATAT TTTAAAGTTT AAAGGTCAGT TTCTCTTAAT CTGATTATGT GCACATATGA 840  
AAATGGCACA TCATATACAT GTAAAATCAG GCAGTATACA TTTATTAATT ACTGTATTTG 900  
ACAAAGGAAA CTCTTAAATT ATAATGTGAA ACCTGGTTTT ATGAAACCAA AGACTAGTGC 960  
AGCATTTTCAG CATATGTAAA AAAAAAAAAA AAGGGAATTG ACATGTCACA TATCAAATGA 1020  
ATGGAAACTT TGTGAAACT TTA AAAAGCA AATTTACTCC AAAGACTTGT ATTGGAAATT 1080  
ACATACCTTT TTTTTTTTTT TTTAAAGGAC TACAGATTAT TTTAATGAC TAAATTGGAG 1140  
TGATACTTCT TACTAAAA ATTATTTCTT AGGCATTCTG AATCTGGGAT GAGAAACAGG 1200  
ATTGTTTCAC AATAGTAAGC ACATAATTTT TAAGGCCAAG GCACATTTGA CTCCTGAGAT 1260  
GAATTTTTTG TGGTCATAAT CAAATACTTA GTTGTTTTTG ATGCCCCAAA ATAAAGTGAG 1320  
AATGGTAATT TGCCAGGAAT TCTTCATAAC AGTATCTTAC AAAAAACGTG TTGCTCTCTT 1380  
CACAGTATTA TGTGTAAAGT CATTGTTTAA AGCACGAATG TTCCCTCTGG GGTACTTGTT 1440  
AAAGCTAAAT TTATTTTGCT TCCCTCCACT TAGAAGTGCT GCACACTTTA CAGCAGCTTC 1500  
CTTTCTTTCC ATGGCACTGC CTAGTTAACA GAAGTCTTAT AAAAATTTAA AAAGACACAT 1560  
TTCTTACAAA AAAGAGTTGA ATGAGGTAAA ATGGCATTAG ATGGCTCTAT ATTTTTTAAA 1620  
GCTATGTAAT TGTTCAGCGT CACTTTTCTA AGTACTTATA CATATCTAAA CATGTCTTCA 1680  
TGGTTTATAT TTTCATTAT ATATGCTGGG CTGGATTAAG CTTTGTTGTG ATTGTGACCA 1740  
ACATTCAGGC CACGTGAGCA CTGTCTTATC ACATCGCCAA TTAGTTGTAA TAAACGTTCA 1800  
ACGTACAAAC ACTGGAGTGT GTTTTTATCT CTTTCCAAAA GTTTGTCAAA CTATGCAGAG 1860  
CTGCTGAAGG AAGAATTTCT CATTTTTTTT TCAGTAAAT GTTGAAAATT CCCCTCCATT 1920  
TGAATATGGT GGTGTTTATA AGCACACACA AGATACATGG TGGAAGATCT AG 1972

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1741 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: THP1AZS08  
(B) CLONE: 2753496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138 :

CGGGTTCCGG GCTCCGGGCT CTGGGTGGCG GCGGCTGTGA GCNGCGGCTG ANCCNCCGCG 60  
CTGCGCANCG ACGCGGGAAT GAAGCGGGCG CTGGGCAGGC GAAAGGGCGT GTGGTTGCGC 120  
CTGAGGAAGA TACTTTTCTG TGTTTTGGGG TTGTACATTG CCATTCCATT TCTCATCAAA 180  
CTATGTCCTG GAATACAGGC CAAACTGATT TTCTTGAATT TCGTAAGAGT TCCCTATTTT 240  
ATTGATTTGA AAAAACCACA GGATCAAGGT TTGAATCACA CGTGTAAC TA CTACCTGCAG 300  
CCAGAGGAAG ACGTGACCAT TGGAGTCTGG CACACCGTCC CTGCAGTCTG GTGGAAGAAC 360  
GCCCCAAGGCA AAGACCAGAT GTGGTATGAG GATGCCTTGG CTTCCAGCCA CCCTATCATT 420  
CTGTACCTGC ATGGGAACGC AGGTACCAGA GGAGGCGACC ACCGCGTGGA GCTTTACAAG 480  
GTGCTGAGTT CCCTTGTTA CCATGTGGTC ACCTTTGACT ACAGAGGTTG GGGTGACTCA 540  
GTGGGAACGC CATCTGAGCG GGGCATGACC TATGACGCAC TCCACGTTTT TGA CTGGATC 600  
AAAGCAAGAA GTGGTGACAA CCCC GTGTAC ATCTGGGGCC ACTCTCTGGG CACTGGCGTG 660  
GCGACAAATC TGGTGCGGCG CCTCTGTGAG CGAGAGACGC CTCCAGATGC CCTTATATTG 720  
GAATCTCCAT TACTAATAT CCGTGAAGAA GCTAAGAGCC ATCCATTTT AGTGATATAT 780  
CGATACTTCC CTGGGTTTGA CTGGTTCTTC CTTGATCCTA TTACAAGTAG TGGAATTAAA 840  
TTTGCAAATG ATGAAAACGT GAAGCACATC TCCTGTCCCC TGCTCATCCT GCACGCTGAG 900  
GACGACCCGG TGGTGCCCTT CCAGCTTGGC AGAAAGCTCT ATAGCATCGC CGCACCAGCT 960  
CGAAGCTTCC GAGATTTCAA AGTTCAGTTT GTGCCCTTTC ATTCAGACCT TGGCTACAGG 1020  
CACAAATACA TTTACAAGAG CCCTGAGCTG CCACGGATAC TGAGGGAATT CCTGGGGAAG 1080  
TCGGAGCCTG AGCACCAGCA CTGAGCCTGG CCGTGGGAAG GAAGCATGAA GACCTCTGCC 1140  
CTCCTCCCGT TTTCTCCAG TCAGCAGCCC GGTATCCTGA AGCCCCGGGG GGCCGGCACC 1200  
TGCAATGCTC AGGAGCCCAG CTCGCACCTG GAGAGCACCT CAGATCCCAG GTGGGGAGGC 1260  
CCCTGCAGGC CTGCAGTGCC CGGAGGCCTG AGCATGGCTG TGTGGAAAGC GTGGGTGGCA 1320  
GGCATGTGGC TCTCCTTGCC GCCCTCAAC CTGAGATCTT GTTGGGAGAC TTAATGGCAG 1380  
CAGGCAGCCA TACTGCCTG GTTGATGCTG CACTGAGCTG GACAGGGGGA GTCCGGGCAG 1440  
GGGACTCTTG GGGCTCGGGA CCATGCTGAG CTTTTTGGCA CCACCCACAG AGAACGTGGG 1500

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GTCCAGGTTC TTTCTGCACC TTCCCAGCAC ATGCAGAATG ACTCCAGTGG TTCCATCGTC 1560  
CCCTCCTGCC CTGTGTACCT GCTTGCCTTT CTCAGCTGCC CCACCTCCCC TGGGCTGGCC 1620  
CACTCACCCA CAGTGGAAGT GCCCGGGATC TGCACTTCCT CCCCTTTCAC CTACCTGTAC 1680  
ACCTAACCTG GCCTTAGACT GAGCTTTATT TAAGAATAAA ATCGTGGTGG TGAACAAAAA 1740  
A 1741

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2808 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARTUT03
- (B) CLONE: 2781553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139 :

GGCAAGATGG CGGAAGGGGA GGACGTGGGA TGGTGGCGGA GCTGGCTGCA GCAGAGCTAC 60  
CAAGCAGTCA AAGAGAAGTC CTCTGAAGCC TTGGAGTTTA TGAAGCGGGA CCTGACGGAG 120  
TTTACCCAGG TGGTGCAGCA TGACACGGCC TGTACCATCG CAGCCACGGC CAGCGTGGTC 180  
AAGGAGAAGC TGGCTACGGA AGGCTCCTCA GGAGCAACAG AGAAGATGAA GAAAGGGTTA 240  
TCTGACTTCC TAGGGGTGAT CTCAGACACC TTTGCCCCCTT CGCCAGACAA AACCATCGAC 300  
TGCGATGTCA TCACCCTGAT GGGCACACCG TCTGGCACAG CTGAGCCCTA TGATGGCACC 360  
AAGGCTCGCC TCTATAGCCT GCAGTCGGAC CCAGCAACCT ACTGTAATGA ACCAGATGGG 420  
CCCCCGGAAT TGTTTGACGC CTGGCTTTCC CAGTTCTGCT TGGAGGAGAA GAAGGGGGAG 480  
ATCTCAGAGC TCCTTG TAGG CAGCCCCTCC ATCCGGGGCC TCTACACCAA GATGGTTCCA 540  
GCAGCTGTTT CCCATTGAGA ATTCTGGCAT CGGTATTTCT ATAAAGTCCA TCAGTTAGAG 600  
CAGGAGCAGG CCCGGAGGGA CGCCCTGAAG CAGCGGGCGG AACAGAGCAT CTCTGAAGAG 660  
CCCGGCTGGG AGGAGGAGGA AGAGGAGCTC ATGGGCATTT CACCCATATC TCCAAAAGAG 720  
GCAAAGGTTC CTGTGGCCAA AATTTCTACA TTCCCTGAAG GAGAACCTGG CCCCAGAGC 780  
CCCTGTGAAG AGAATCTGGT GACTTCAGTT GAGCCCCCAG CAGAGGTGAC TCCATCAGAG 840  
AGCAGTGAGA GCATCTCCCT CGTGACACAG ATCGCCAACC CGGCCACTGC ACCTGAGGCA 900  
CGAGTGCTAC CCAAGGACCT GTCCCAAAAG CTGCTAGAGG CATCCTTGGA GGAACAGGGC 960  
CTGGCTGTGG ATGTGGGTGA GACTGGACCC TCACCCCTA TCACTCCAA GCCCCTAACG 1020

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CCTGCTGGCC ACACCGGCGG CCCAGAGCCC AGGCCTCCAG CCAGAGTAGA GACTCTGAGG 1080  
GAGGAGGCGC CCACAGACTT ACGGGTGTTT GAGCTGAACT CGGATAGTGG GAAGTCTACA 1140  
CCCTCCAACA ATGGAAAGAA AGGCTCAAGC ACGGACATCA GTGAGGACTG GGAGAAAGAC 1200  
TTTGACTTGG ACATGACTGA AGAGGAGGTG CAGATGGCAC TTTCCAAAGT GGATGCCTCC 1260  
GGGGAGCTGG AAGATGTAGA GTGGGAGGAC TGGGAGTGAG GGAGCCAGAG GGAGCAGCTC 1320  
CCCCACCCAT GGCATCTCTC GCCTCCCTCG CTCGTCTCAG CCCAGCCCTG GAAGACTGAG 1380  
AATGTTCCCC CAAATCTCCT CTGCCAACCA GAGCTCTGGG CACAGATTCT GGTGGCTCCC 1440  
TGCTGGCCCT CTTGGGCCTC TGCTCACACC TGGGAAGGGG CTCTCTAAAT CCCGGCCAGA 1500  
AACTCTGACT TGTGCCAACA ATAGGATGAC CCAAGGGAGA GGAAACCTAT CCTCCTCACC 1560  
AGAAGAGCCT GTGTTTTTCT GCTGAACACC CACTGTTCCT GAGGACTCCT GCTGGGAAGT 1620  
CCCAAGGGAT AGTTCTAGCC CTTCTGCCTG TGTAGACAGA AGCTAAACCA CCAGTCTCTC 1680  
TCGGAGGAAG CTGAGACAAC ATACTCTGTC CATACATAAG CAGGCAGGGA GGGCCATGCC 1740  
ACCTACCCTT GGCTAAACAG GGACAGTGAA CACATTTTGG TTCCTATCCC AGTGGGTAAG 1800  
AGGCACTTAT CTCTGGGAAA TTTGCCTCTC TTGGGACTCT CCCCCTCCA GGCATTTTCC 1860  
ATTCCTGGAA AGGCTCCTTT GGGGTTTCTG ATCCAGAGAC CAAACCCTGA CCCACCTCCT 1920  
TCCTTTCTC CAGCCCACGC TGGTCTGTCC CCATGCCTTC CCAGGGCTTC TTCATGTCAG 1980  
ATGCACCCAA GTCCTTAGCC CAGCTGTGCC ACCTGCAGGA GTTCGCTCTT GCGTTTCTTC 2040  
CCCTCCCCAA GAAGGGAGGG GGCTACTTCA GGCCCTTCTG TGTGTTGCCT GGCAGGATAC 2100  
CTTGTTCCAA CAGCTACCCA CCTCAACTCC CCTGTAGTTT AGGACACAAA ACAGCTACCA 2160  
GCGGTACAGA GCGGTGATCA AAGCCGAGTA CTTACAATCT TGGTAAGCCT AGCTTCTCCG 2220  
CCTCAGCCCT TCTGCTTCTG GAAGGGCTAT CCTGGGGGTG AACTTGAAAC TCTCATCAGG 2280  
CTTCTGCAAA AGCTCTTCTT CCTGAAGACA GACCCAGCCT TTGTGCTCTC ACCCTCCACT 2340  
CTGGTAAAGC TGCACCTCTG GGGGAATGAG GGGCTGCAGG AATCTCTGGA GAGCCTGGTG 2400  
CTTCACGATG CTGCTCTGGT GATTCTTGTA CCTAATCTGG TGTGCTCACC AATGAGTGAA 2460  
AGGGATCGTG GGTGAGGGAC ACCGAGAGAG TGAGGTCACT TCCACTTCAA ACCTTCAGTG 2520  
AGGGGGTGGG ATGGAGAGAA TGCTGAATCT TTTTTTTGAC GGGATGGGGT TTTTCTCTTT 2580  
GTAATTATTT CTTTAGTTTA ATTAACCTTT TGGTTGTTTG TGCAATATTA TATATTTTAA 2640  
ATTATAATGC ATCTCCCCAG AGTATTTTGT AGCTGGGAAA AGAAAAAGG AAAAAAGAA 2700  
AAAAAGATTC TAACAGCTGT TAGTTTTATA ATTAAAAAAG AAAGAAAAAA GAACCTTGTC 2760  
CTGAACCTTT TACAGACTTG CCGTTAACAG CATTAAAGTG ATTCACCC 2808

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 717 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
    (A) LIBRARY: ADRETUT06  
    (B) CLONE: 2821925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140 :

CATGCGCCGA CCTTCCTCGG CTGGATTTAC ANGTTNNCCC TTAACACCCG GGATTTAAGG 60  
GACCCACACT ACCTTCCCGA AGTTGAAGGC AAGCGGTGAT TGTTTGTAGA CGGCGCTTTG 120  
TCATGGGACC TGTGCGGTTG GGAATATTGC TTTTCCTTTT TTTGGCCGTG CACGAGGCTT 180  
GGGCTGGGAT GTTGAAGGAG GAGGACGATG ACACAGAACG CTTGCCCAGC AAATGCGAAG 240  
TGTGTAAGCT GCTGAGCACA GAGCTACAGG CGGAACTGAG TCGCACCGGT CGATCTCGAG 300  
AGGTGCTGGA GCTGGGGCAG GTGCTGGATA CAGGCAAGAG GAAGAGACAC GTGCCTTACA 360  
GCGTTTCAGA GACAAGGCTG GAAGAGGCCCT TAGAGAATTT ATGTGAGCGG ATCCTGGACT 420  
ATAGTGTTCA CGCTGAGCGC AAGGGCTCAC TGAGATATGC CAAGGGTCAG AGTCAGACCA 480  
TGGCAACACT GAAAGGCCTA GTGCAGAAGG GGGTGAAGGT GGATCTGGGG ATCCCTCTGG 540  
AGCTTTTGGG ATGAGCCCAG CCGTTGAGGT CACATACCTC AAGAAGCAGT GTGAGACCAT 600  
GTTNGAGGAG TTTTGAGACA TTGTGGGAGA CTGGTACTTG CACCATCAGG AGCAGCCGCT 660  
ACAAGATTTT CTCTGTGAAG GTCATGTGCT GCCAGCTGCT TGAAGTGCAT GTCGGGT 717

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 2552 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
    (A) LIBRARY: UTRSTUT05  
    (B) CLONE: 2879068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141 :

GGCAGGGGGC GCGCCGGGCC CAGCGCCACG TCACCGCCCA GCAGCCCTCC CGATTGGCGG 60  
GCGGGGCGGC TATAAAGGGA GGGCGCAGGC GGCGCCCGGA TCTCTTCCGC CGCCATTTTA 120

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AATCCAGCTC CATAACAACGC TCCGCCGCCG CTGCTGCCGC GACCCGGACT GCGCGCCAGC 180  
ACCCCCCTGC CGACAGCTCC GTCACATATGG AGGATATGAA CGAGTACAGC AATATAGAGG 240  
AATTCGCAGA GGGATCCAAG ATCAACGCGA GCAAGAATCA GCAGGATGAC GGTAAAATGT 300  
TTATTGGAGG CTTGAGCTGG GATACAAGCA AAAAAGATCT GACAGAGTAC TTGTCTCGAT 360  
TTGGGGAAGT TGTAGACTGC ACAATTAAAA CAGATCCAGT CACTGGGAGA TCAAGAGGAT 420  
TTGGATTTGT GCTTTTCAAA GATGCTGCTA GTGTTGATAA GGTTTTGGAA CTGAAAGAAC 480  
ACAACTGGA TGGCAAATTG ATAGATCCCA AAAGGGCCAA AGCTTTAAAA GGGAAAGAAC 540  
CTCCCAAAAA GGTTTTTGTG GGTGGATTGA GCCCGGATAC TTCTGAAGAA CAAATTAAAG 600  
AATATTTTGG AGCCTTTGGA GAGATTGAAA ATATTGAACT TCCCATGGAT AAAAAACAA 660  
ATGAAAGAAG AGGATTTTGT TTTATCACAT ATACTGATGA AGAGCCAGTA AAAAAATTGT 720  
TAGAAAGCAG ATACCATCAA ATTGGTTCTG GGAAGTGTGA AATCAAAGTT GCACAACCCA 780  
AAGAGGTATA TAGGCAGCAA CAGCAACAAC AAAAAGGTGG AAGAGGTGCT GCAGCTGGTG 840  
GACGAGGTGG TACGAGGGGT CGTGGCCGAG GTCAGGGCCA AACTGGAAC CAAGGATTTA 900  
ATAACTATTA TGATCAAGGA TATGGAAATT ACAATAGTGC CTATGGTGGT GATCAAACT 960  
ATAGTGGCTA TGGCGGATAT GATTATACTG GGTATAACTA TGGGAACATAT GGATATGGAC 1020  
AGGGATATGC AGACTACAGT GGCCAACAGA GCACTTATGG CAAGGCATCT CGAGGGGGTG 1080  
GCAATCACCA AAACAATTAC CAGCCATACT AAAGGAGAAC ATTGGAGAAA ACAGGTGTGT 1140  
ATAAGAGTAC AGGAAAACAG TAGAAATGTC TAATTTAATT TAAAGATCAA TAGACAAATG 1200  
AAACGTAAAA ACAAATACT ATGTAGCCTG TTTTACTAA ATTGTTGATT TTTTAATTGC 1260  
TTTATGAGCC TGTTTTGCCT AAAGTGTCTA TAGATCTTTA ACTTTAAAGT CTTATCTCAC 1320  
TTTCTTTAGT ATTGCAGAAA AACTTAAGAG TTTTCTGTT TGCTTTTGTG TACCAGGTGG 1380  
TCTAGAGGAA TAATTAAACA TTTTAGAACT ATTAACAGGT AAAGTACTGA AATGGGTACA 1440  
ACTTAAGGAA AACAAGAATG TTGTCTTCTA ACTCTGACAT TATACCTTGT TTGTACCCGC 1500  
CAGCGGGAAC TTCATTGCAG GCCGTGTGTC ACCCTGACCA CGTCTATCTC TGGGGGTCGC 1560  
ACGTTGCGGG CAGAGCGCAA GGCATACACC AGAAAACGCT GTCCTGTGGT ATGGTCTCTT 1620  
CCAAC TTCAT GTACCAGCGT AAAGATTAAA GTGGAAAAC TCAGACTTTG GCTTCATTTT 1680  
TAATCTTTTT GGAGATTAAG TGTCTAACT TAACTTAAAT GGTTTTTTAC AGGAGTTAAA 1740  
GTACATAAAT GCCTTTTTTAC AGCTTAATCA TTTTGGTCTT CTGTTTAGTG TTGTATTTCA 1800  
ATTGTGGAGC CTCATTTTAA GTGTTCATTC TTTTAAGATT TAATGCTTGC TTTTCTTTT 1860  
TATAGCTAAT AGTGAAATCT ACAAACCAA ACAAGAACTT TTAAATCTGG GATATAAATT 1920  
AAAGATCATA TGCACAGATC AATTTATGTT CTTGTAATAA ACTTATTAGA AATTGGTGTT 1980

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TGTGATAGCA TTTTACTTGG GTTACTAGAG ATGCTTCTAG TAGACCTTAA TCTAGCATAG 2040  
TTGAACCTCT GAATATGGGA AGGTTGTATT CCCAGATTCT TTCCTGAATA GATTTGAATT 2100  
TAATGTCATT TGGGAACTCC AGGGTGAGTT TATTGACTAC CCAAACCTGTA TTTTACCAAT 2160  
AAATATGCAT ATGATCTTTA ATTATTGAAG AAAATAAAGT GAGGACTTAA AACAATTCAT 2220  
GAAAGTGGAC CTTTAAAAGC TTGTCAGAGT TGCACAAATC TAACTGGTAT TTTGTTTTTG 2280  
TTTTTAGGAG GAGATGTTAA AGTAACCCAT CTTGCAGGAC GACATTGAAG ATTGGTCTTC 2340  
TGTTGATCTA AGATGATTAT TTTGTAAAAG ACTTTCTAGT GTACAAGACA CCATTGTGTC 2400  
CAACTGTATA TAGCTGCCAA TTAGTTTTCT TTGTTTTTAC TTTGTCCTTT GCTATCTGTG 2460  
TTATGACTCA ATGTGGATTT GTTTATACAC ATTTTATTG TATCATTTCA TGTTAAACCT 2520  
CAAATAAATG CTTCCTTATG TGAAAAA AAAA 2552

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1046 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SINJNOT02
- (B) CLONE: 2886757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142 :

TACCAGTGTA AAGCCAGAGC TGAGGTTCTT GATAGTCCAC AATGGGTGAA CCACAGCAAG 60  
TGAGTGCACCT TCCACCACCT CCAATGCAAT ATATCAAGGA ATATACGGAT GAAAATATTC 120  
AAGAAGGCTT AGCTCCCAAG CCTCCCCCTC CAATAAAAGA CAGTTACATG ATGTTTGGCA 180  
ATCAGTTCCA ATGTGATGAT CTTATCATCC GCCCTTTGGA AAGTCAGGGC ATCGAACGGC 240  
TTCATCCTAT GCAGTTTGAT CACAAGAAAG AACTGAGAAA ACTTAATATG TCTATCCTTA 300  
TTAATTTCTT GGACCTTTTA GATATTTTAA TAAGGAGCCC TGGGAGTATA AAACGAGAAG 360  
AGAAACTAGA AGATCTTAAG CTGCTTTTTG TACACGTGCA TCATCTTATA AATGAATACC 420  
GACCCACCA AGCAAGAGAG ACCTTGAGAG TCATGATGGA GGTCCAGAAA CGTCAACGGC 480  
TTGAAACAGC TGAGAGATTT CAAAAGCACC TGGAACGAGT AATTGAAATG ATTCAGAATT 540  
GCTTGGCTTC TTTGCCTGAT GATTTGCCTC ATTCAGAAGC AGGAATGAGA GTAAAACTG 600  
AACCAATGGA TGCTGATGAT AGCAACAATT GTACTGGACA GAATGAACAT CAAAGAGAAA 660  
ATTCAGGTCA TAGGAGAGAT CAGATTATAG AGAAAGATGC TGCCTTGTGT GTCCTAATTG 720



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ATGAGATGAA TGAAAGACCA TGAAAGATGT TTCTTTTTCT TTTTTCCTT TTGATAATAG 780  
CATCATATAT TAGTTCATTT TCTTTTGGAC AGTCTTAAGA GAAGTTTCAC TAAAAATGTA 840  
AACAGCTTTA ATCTTGACTC CAAATTTTTC AATTATGAGA TGTCATAGGC AGTAATTTTCG 900  
CTGTATAACA AGCATAGACA AATGAGTGTC CCTGCACTAA GAAGAATCAC TTTAAAAAGC 960  
AAAGTGTTAG CTGCTGTTGT ATGGGACATT CCTATGTTTT AGAGTTGCAG TAAAACTTTG 1020  
ATGATAACCT CAAAAAAAAA TAAAAA 1046

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SCORNOT04
- (B) CLONE: 2964329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143 :

GCCCTGGGCT CGCGGCGGTG CCGCGGGGAT GGCGGGAGCC GGAGCTGGAG CCGGAGCTCG 60  
CGGCGGAGCG GCGGCGGGGG TCGAGGCTCG AGCTCGCGAT CCACCGCCCG CGCACCGCGC 120  
ACATCCTCGC CACCCTCGGC CTGCGGCTCA GCCCTCGGCC CGCAGGATGG ATGGCGGGTC 180  
AGGGGGCCTG GGGTCTGGGG ACAACGCCCC GACCACTGAG GCTCTTTTCG TGGCACTGGG 240  
CGCGGGCGTG ACGGCGCTCA GCCATCCCCT GCTCTACGTG AAGCTGCTCA TCCAGGTGGG 300  
TCATGAGCCG ATGCCCCCA CCCTTGGGAC CAATGTGCTG GGGAGGAAGG TCCTCTATCT 360  
GCCGAGCTTC TTCACCTACG CCAAGTACAT CGTGCAAGTG GATGGTAAGA TAGGGCTGTT 420  
CCGAGGCCTG AGTCCCCGGC TGATGTCCAA CGCCCTCTCT ACTGTGACTC GGGGTAGCAT 480  
GAAGAAGGTT TTCCCTCCAG ATGAGATTGA GCAGTTTCC AACAAGGATG ATATGAAGAC 540  
TTCCCTGAAG AAAGTTGTGA AGGAGACCTC CTACGAGATG ATGATGCAGT GTGTGTCCCG 600  
CATGTTGGCC CACCCCTGC ATGTCATCTC AATGCGCTGC ATGGTCCAGT TTGTGGGACG 660  
GGAGGCCAAG TACAGTGGTG TGCTGAGCTC CATTGGGAAG ATTTTCAAAG AGGAAGGGCT 720  
GCTGGGATTC TTCGTTGGAT TAATCCCTCA CCTCCTGGGC GATGTGGTTT TCTTGTGGGG 780  
CTGTAACCTG CTGGCCCACT TCATCAATGC CTACCTGGTG GATGACAGCT TCAGCCAGGC 840  
CCTGGCCATC CGGAGCTATA CCAAGTTCGT GATGGGGATT GCAGTGAGCA TGCTGACCTA 900  
CCCCCTCCTG CTAGTTGGCG ACCTCATGGC TGTGAACAAC TCGGGGCTGC AAGCTGGGCT 960

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CCCCCCTTAC TCCCCAGTGT TCAAATCCTG GATTCACTGC TGGAAGTACC TGAGTGTGCA 1020  
GGGCCAGCTC TTCCGAGGCT CCAGCCTGCT TTTCCGCCGG GTGTCATCAG GATCGTGCTT 1080  
TGCCCTGGAG TAACCTGAAT CATCTAAAAA ACACGGTCTC AACCTGGCCA CCGTGGGTGA 1140  
GGCCTGACCA CCTTGGGACA CCTGCGAGAC GACTCCAACC CAACAACAAC CAGATGTGCT 1200  
CCAGCCCAGC CGGGCTTCAG TTCCATATTT GCCATGTGTC TGTCCAGATG TGGGGTTGAG 1260  
CGGGGGTGGG GCTGCACCCA GTGGATTGGG TCACCCGGCA GACCTAGGGA AGGTGAGGCG 1320  
AGGTGGGGAG TTGGCAGAAT CCCCATACCT CGCAGATTG CTGAGTCTGT CTTGTGCAGA 1380  
GGGCCAGAGA ATGGCTTATG GGGGCCCAGG TTGGATGGGG AAAGGCTAAT GGGGTCAGAC 1440  
CCCACCCCGT CTACCCCTCC AGTCAGCCCA GCGCCCATCC TGCAGCTCAG CTGGGAGCAT 1500  
CATTCTCCTG CTTTGTACAT AGGGTGTGGT CCCCTGGCAC GTGGCCACCA TCATGTCTAG 1560  
GCCTATGCTA GGAGGCAAAT GGCCAGGCTC TGCCTGTGTT TTTCTCAACA CTACTTTTCT 1620  
GATATGAGGG CAGCACCTGC CTCTGAATGG GAAATCATGC AACTACTCAG AATGTGTCTT 1680  
CCTCATCTAA TGCTCATCTG TTTAATGGTG ATGCCTCGCG TACAGGATCT GGTTACCTGT 1740  
GCAGTTGTGA ATACCAGAG GTTGGGCAGA TCAGTGTCTC TAGTCCTACC CAGTTTTAAA 1800  
GTTTCATGGTA AGATTGACC TCATCTCCCG CAAATAAATG TATTGGTGAT TTGGAAAAAA 1860  
AAAA 1864

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SCORNOT04
- (B) CLONE: 2965248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144 :

GTCTGCAGCT CCGGCCGCCA CTTGCGCCTC TCCAGCCTCC GCAGGCCCAA CCGCCGCCAG 60  
CACCATGGCC AGCACCATTT CCGCCTACAA GGAGAAGATG AAGGAGCTGT CCGTGCTGTC 120  
GCTCATCTGC TCCTGCTTCT ACACACAGCC GCACCCCAAT ACCGTCTACC AGTACGGGGA 180  
CATGGAGGTG AAGCAGCTGG ACAAGCGGGC CTCAGGCCAG AGCTTCGAGG TCATCCTCAA 240  
GTCCCCTTCT GACCTGTCCC CAGAGAGCCC TATGCTCTCC TCCCCACCA AGAAGAAGGA 300  
CACCTCCCTG GAGGAGCTGC AAAAGCGGCT GGAGGCAGCC GAGGAGCGGA GGAAGACGCA 360

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GGAGGCGCAG GTGCTGAAGC AGCTGGCGGA CGGCGCGAGC ACGAGCGCGA GGTGCTGCAC 420  
AAGGCGCTGG AGGAGAATAA CAACTTCAGC CGCCAGGCGG AGGAGAAGCT CAACTACAAG 480  
ATGGAGCTCA GCAAGGAGAT CCGCGAGGCA CACCTGGCCG CACTGCGCGA GCGGCTGCGC 540  
GAGAAGGAGC TGCACGCGGC CGAGGTGCGC AGGAACAAGG AGCAGCGAGA AGAGATGTCTG 600  
GGCTAAGGGC CCGGGACGGG CGGCGCCCAT CCTGCGACGG AACACGTTCG GGTTTTGGTT 660  
TTGTTTCGTT CACCTCTGTC TAGATGCAAC TTTTGTTCCT CCTCCCCAC CCCAGCCCCC 720  
AGCTTCATGC TTCTCTTCCG CACTCAGCCG CCCTGCCCTG TCCTCGTGGT GAGTCGCTGA 780  
CCACGGCTTC CCCTGCAGGA GCCGCCGGGC GTGAGACGCG GTCCCTCGGT GCAGACACCA 840  
GGCCGGGCGC GGCTGGGTCC CCCGGGGGCC CTGTGAGAGA GGTGGTGGTG ACCGTGGTAA 900  
ACCCAGGGCG GTGGCGTGGG ATCGCGGGTC CTTACGCTGG GCTGTCTGGT CAGCACGTGC 960  
AGGTCAGGGC AGGTCCTCTG AGCCGGCGCC CCTGGCCAGC AGGCGAGGCT ACAGTACCTG 1020  
CTGTCTTTCC AGGGGAAGG GGCTCCCCAT GAGGGAGGGG CGACGGGGGA GGGGGGTGAT 1080  
GGTGCTGGG AGCCTGCGTG TGCAGCCGGT GCTTGTGAA CTGGCAGGCG GGTGGGTGGG 1140  
GGCTGCAGCT TTCCTTAATG TGGTTGCACA GGGTCTCTT GAGACCACCT GGCGTGAGGT 1200  
GGACACCCTG GGCCTTCCTG GAAGCCTGCA GTTGGGGGCC TGCCCTGAGT CTGCTGGGGA 1260  
GTGGGCATTC TCTGCCAGGG ACCCATGAGC AGGCTGCATG GTCTAGAGGT TGTGGGCAGC 1320  
ATGGACAGTC CCCCACTCAG AAGTGCAAGA GTTCCAAAGA GCCTCTGGCC CAGGCCCCCTC 1380  
CGTGGGACAG CCCCGCCGCC CCTCCCCACC AGGGCTTTGC AGATGTCCTT GAAAGACCCA 1440  
CCCTAGAGCC CTTTGAGTG CTGGCCCCCTC CTGTGCCCTC TGCCCTGGTG GAAGCGGCAG 1500  
CCACAAGTCC TCCTCAGGGA GCCCCAAGGG GGATTTTGTG GGACCGCTGC CCACAGATCC 1560  
AGGTGTTGGA AGGGCAGCGG GTAAGGTTCC CAAGCCAGCC CCAACACCCT TCCCACTTGG 1620  
CACCCAGAGG GGGCTGTGGG TGGAGGCCTG ACTCCAGGCC TCTCCTGCCC ACACCCTCTG 1680  
GGCTGAGTTC CTTCTTTCCC TTGGACGCCC AGTGCTGGCC TTGGAGGACG GTCAGCTGGA 1740  
GGATGGCGGT GGGGGAGGCT GTCTTTGTAC CACTGCAGCA TCCCCACTT CTCCACGGAA 1800  
GCCCCATCCC AAAGCTGCTG CCTGGCCCCCT TGCTGTAAAG TGTGAAGGGG GCGGCTGAGT 1860  
TCTCTTAGGA CCCAGAGCCA GGGCCCTCAA CTTCCATCCT GCGGGAGGCC TTGGCCGGGC 1920  
ACTGCCAGTG TCTTCCAGAG CCACACCCAG GGACCACGGG AGGATCCTGA CCCCTGCAGG 1980  
GCTCAGGGGT CAGCAGGGAC CCACTGCCCC ATCTCCCTCT CCCACCAAG ACAGCCCCAG 2040  
AAGGAGCAGC CAGCTGGGAT GGGAAACCAA GGCTGTCCAC ATCTGGCTTT TGTGGGACTC 2100  
AGAAAGGGAA GCAGAACTGA GGGCTGGGAT ATCCTCATG GTGGCAGCGC TCATAGCGAA 2160  
AGCCTACTGT AATATGCACC CATCTCATCC ACGTAGTAAA GTGAACTTAA AAATTCAATC 2220

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AAATGAACAA TTAAATAAAC ACCTGTGTGT TTAAGACAAA ATAAAAATGG AGGAGAACAA 2280  
AAAAAAAGGG GCGGT 2295

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TLYMNOT06
- (B) CLONE: 3000534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145 :

CGGGGACGGA AGCAGCCCCT GGGCCCGAGG GGCTCGAGGC CGGGCCGGGG CGATGTGGAG 60  
CGCGGGCCGC GCGGGGGCTG CCTGGCCGGT GCTGTTGGGG CTGCTGCTGG CGCTGTTAGT 120  
GCCGGGCGGT GGTGCCGCCA AGACCGGTGC GGAGCTCGTG ACCTGCGGGT CGGTGCTGAA 180  
GCTGCTCAAT ACGCACCACC GCGTGC GGCT GCACTCGCAC GACATCAAAT ACGGATCCGG 240  
CAGCGGCCAG CAATCGGTGA CCGGCGTAGA GGCGTCGGAC GACGCCAATA GCTACTGGCG 300  
GATCCGCGGC GGCTCGGAGG GCGGGTGCCC GCGCGGGTCC CCGGTGCGCT GCGGGCAGGC 360  
GGTGAGGCTC ACGCATGTGC TTACGGGCAA GAACCTGCAC ACGCACCCT TCCCGTCGCC 420  
GCTGTCCAAC AACCAGGAGG TGAGTGCCTT TGGGGAAGAC GGCGAGGGCG ACGACCTGGA 480  
CCTATGGACA GTGCGCTGCT CTGGACAGCA CTGGGAGCGT GAGGCTGCTG TGCGCTTCCA 540  
GCATGTGGGC ACCTCTGTGT TCCTGTCACT CACGGGTGAG CAGTATGGAA GCGGATCCG 600  
TGGGCAGCAT GAGGTCCACG GCATGCCCAG TGCCAACACG CACAATACGT GGAAGGCCAT 660  
GGAAGGCATC TTCATCAAGC CTAGTGTGGA GCCCTCTGCA GGTCACGATG AACTCTGAGT 720  
GTGTGGATGG ATGGGTGGAT GGAGGGTGGC AGGTGGGGCG TCTGCAGGGC CACTCTTGGC 780  
AGAGACTTTG GGTGTGTAGG GGTCCTCAAG TGCCTTTGTG ATTAAAGAAT GTTGGTCTAA 840  
AA 842

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2345 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: HEAANOT01  
(B) CLONE: 3046870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146 :

GTCCCGCCCC GCAGCTGCGC GCAGGCGCTC GACGAGCCGC TCGCATTCTA CGTAACGGAC 60  
GGCGGAGGCT ACGTGAAGAG AGGCGCGGCG TGA CTGAGCT ACGGTTCTGG CTGCGTCCTA 120  
GAGGCATCCG GGGCAGTAAA ACCGCTGCGA TCGCGGAGGC GGCGGCCAGG CCGAGAGGCA 180  
GGCCGGGCGAG GGGTGTCTGA CGCAGGGCGC TGGGCGGGGT TTCGGCTTCG GCCACAGCTT 240  
TTTTTCTCAA GGTGCAATGA AAGCCTTCCA CACTTTCTGT GTTGTCTTC TGGTGTCTTG 300  
GAGTGTCTCT GAAGCCAAGT TTGATGATTT TGAGGATGAG GAGGACATAG TAGAGTATGA 360  
TGATAATGAC TTCGCTGAAT TTGAGGATGT CATGGAAGAC TCTGTTACTG AATCTCCTCA 420  
ACGGGTCATA ATCACTGAAG ATGATGAAGA TGAGACCACT GTGGAGTTGG AAGGGCAGGA 480  
TGAAAACCAA GAAGGAGATT TTGAAGATGC AGATACCCAG GAGGGAGATA CTGAGAGTGA 540  
ACCATATGAT GATGAAGAAT TTGAAGGTTA TGAAGACAAA CCAGATACTT CTTCTAGCAA 600  
AAATAAAGAC CCAATAACGA TTGTTGATGT TCCTGCACAC CTCCAGAACA GCTGGGAGAG 660  
TTATTATCTA GAAATTTTGA TGGTGA CTGCTGCT TATATCATGA ATTACATCAT 720  
TGGGAAGAAT AAAAACAGTC GCCTTG CACA GGCCTGGTTT AACACTCATA GGGAGCTTTT 780  
GGAGAGCAAC TTTACTTTAG TGGGGGATGA TGGA ACTAAC AAAGAAGCCA CAAGCACAGG 840  
AAAGTTGAAC CAGGAGAATG AGCACATCTA TAACCTGTGG TGTCTGGTC GAGTGTGCTG 900  
TGAGGGCATG CTTATCCAGC TGAGGTTCTT CAAGAGACAA GACTTACTGA ATGTCCTGGC 960  
CCGGATGATG AGGCCAGTGA GTGATCAAGT GCAAATAAAA GTAACCATGA ATGATGAAGA 1020  
CATGGATACC TACGTATTTG CTGTTGGCAC ACGGAAAGCC TTGGT GCGAC TACAGAAAGA 1080  
GATGCAGGAT TTGAGTGAGT TTTGTAGTGA TAAACCTAAG TCTGGAGCAA AGTATGGACT 1140  
GCCGGACTCT TTGGCCATCC TGTCAGAGAT GGGAGAAGTC ACAGACGGAA TGATGGATAC 1200  
AAAGATGGTT CACTTTCTTA CACACTATGC TGACAAGATT GAATCTGTTC ATTTTTCAGA 1260  
CCAGTTCTCT GGTCCAAAAA TTATGCAAGA GGAAGGTCAG CCTTTAAAGC TACCTGACAC 1320  
TAAGAGGACA CTGTTGTTTA CATTTAATGT GCCTGGCTCA GGTAACACTT ACCCAAAGGA 1380  
TATGGAGGCA CTGCTACCCC TGATGAACAT GGTGATTTAT TCTATTGATA AAGCCAAAAA 1440  
GTTCCGACTC AACAGAGAAG GCAAACAAAA AGCAGATAAG AACCGTGCCC GAGTAGAAGA 1500  
GAACTTCTTG AAAGTGACAC ATGTGCAAAG ACAGGAAGCA GCACAGTCTC GGCGGGAGGA 1560

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GAAGAAAAAGA GCAGAGAAGG AGCGAATCAT GAATGAGGAA GATCCTGAGA AACAGCGCAG 1620  
GCTGGAGGAG GCTGCATTGA GGCCTGAGCA AAAGAAGTTG GAAAAGAAGC AAATGAAAAT 1680  
GAAACAAATC AAAGTGAAAG CCATGTAAAG CCATCCCAGA GATTTGAGTT CTGATGCCAC 1740  
CTGTAAGCTC TGAATTCACA GGAAACATGA AAAACGCCAG TCCATTTCTC AACCTTAAAT 1800  
TTCAGACAGT CTTGGGCAAC TGAGAAATCC TTATTTTCATC ATCTACTCTG TTTGGGGTTT 1860  
GGGGTTTTAC AGAGATTGAA GATACCTGGA AAGGGCTCTG TTTCAAGAAT TTTTTTTTCC 1920  
AGATAATCAA ATTATTTTGA TTATTTTATA AAAGGAATGA TCTATGAAAT CTGTGTAGGT 1980  
TTTAAATATT TTAATAATTA TAATACAAAT CATCAGTGCT TTTAGTACTT CAGTGTTTAA 2040  
AGAAATACCA TGAAATTTAT AGGTAGATAA CCAGATTGTT GCTTTTTGTT TAAACCAAGC 2100  
AGTTGAAATG GCTATAAAGA CTGACTCTAA ACCAAGATTC TGCAAATAAT GATTGGAATT 2160  
GCACAATAAA CATTGCTTGA TGTTTTCTTG TATGTCTACA TTAAACTTGA GAAAAAGTAA 2220  
AAATTAGAAC ACTGTATGTA GTAATGAAAT TTCAGGGACC CAGAACATAA TGTAGTATAT 2280  
GTTTTTAGGT GGGAGATGCT GATAACAAAA TTAATAGGAA GTCTGTAGGC ATTAGGATAC 2340  
TGACA 2345

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PONSATZ01
- (B) CLONE: 3057669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147 :

CCCACGCGTC CGCCACGCG TCCGTTTTCA GTAGGGATTT CCTGTGACCA GACAAGTTCA 60  
TCTGAGAGCC AGTTCTCACC ACTGGAATTC TCAGGAATGG ACCATGAGGA CATCAGTGAG 120  
TCAGTGGATG CAGCATACAA CCTCCAGGAC AGTTGCCTTA CAGACTGTGA TGTGGAAGAT 180  
GGGACTATGG ATGGCAATGA TGAGGGGCAC TCCTTTGAAC TTTGTCCTTC TGAAGCTTCT 240  
CCTTATGTAA GGTCAAGGGA GAGAACCTCC TCTTCAATAG TATTTGAAGA TTCTGGCTGT 300  
GATAATGCTT CCAGTAAAGA AGAGCCGAAA ACTAATCGAT TGCATATTGG CAACCATTGT 360  
GCTAATAAAC TAACTGCTTT CAAGCCCACC AGTAGCAAAT CTTCTTCTGA AGCTACATTG 420  
TCTATTTCTC CTCCAAGACC AACCACCTTA AGTTTAGATC TCACTAAAAA CACCACAGAA 480

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AAACTCCAGC CCAGTTCACC AAAGGTGTAT CTTTACATTC AAATGCAGCT GTGCAGAAAA 540  
GAAAACCTCA AAGACTGGAT GAATGGACGA TGTACCATAG AGGAGAGAGA GAGGAGCGTG 600  
TGTCTGCACA TCTTCCTGCA GATCGCAGAG GCAGTGGAGT TTCTTCACAG TAAAGGACTG 660  
ATGCACAGGG ACCTCAAGCC ATCCAACATA TTCTTTACAA TGGATGATGT GGTCAAGGTT 720  
GGAGACTTTG GGTTAGTGAC TGCAATGGAC CAGGATGAGG AAGAGCAGAC GGTTCAGACC 780  
CCAATGCCAG CTTATGCCAG ACACACAGGA CAAGTAGGGA CCAAAGTGTAT TATGAGCCCA 840  
GAGCAGATTC ATGGAAACAG CTATTCTCAT AAAGTGGACA TCTTTTCTTT AGGCCTGATT 900  
CTATTTGAAT TGCTGTATCC ATTCAGCACT CAGATGGAGA GAGTCAGGAC CTTAACTGAT 960  
GTAAGAAATC TCAAATTTCC ACCATTATTT ACTCAGAAAT ATCCTTGTGA GTACGTGATG 1020  
GTTCAAGACA TGCTCTCTCC ATCCCCCATG GAACGACCTG AAGCTATAAA CATCATTGAA 1080  
AATGCTGTAT TTGAGGACTT GGACTTTCCA GGAAAAACAG TGCTCAGACA GAGGTCTCGC 1140  
TCCTTGAGTT CATCGGGAAC AAAACATTCA AGACAGTCCA ACAACTCCCA TAGCCCTTTG 1200  
CCAAGCAATT AGCCTTAAGT TGTGCTAGCA ACCCTAATAG GTGATGCAGA TAATAGCCTA 1260  
CTTCTTAGAA TATGCCTGTC CAAAATTGCA GACTTGAAAA GTTTGTTCTT CGCTCAATTT 1320  
TTTTGTGGAC TACTTTTTTT ATATCAAATT TAAGCTGGAT TTGGGGGCAT AACCTAATTT 1380  
GAGCCAACTC CTGAGTTTTG CTATACTTAA GGAAAGGGCT ATCTTTGTTC TTTGTTAGTC 1440  
TCTTGAAACT GGCTGCTGGC CAAGCTTTAT AGCCCTCACC ATTTGCCTAA GGAGGTAGCA 1500  
GCAATCCCTA ATATATATAT ATAGTGAGAA CTAAAATGGA TATATTTTTA TAATGCAGAA 1560  
GAAGGAAAGT CCCCCTGTGT GGTAAGTGT TGTCTCTAGA AATATGCTTT CTAGAGATAT 1620  
GATGATTTTG AACTGATTT CTAGAAAAAG CTGACTCCAT TTTTGTCCCT GGCGGGTAAA 1680  
TTAGGAATCT GCACTATTTT GGAGGACAAG TAGCACAAAC TGTATAACGG TTTATGTCCG 1740  
TAGTTTTATA GTCCTATTTG TAGCATTCAA TAGCTTTATT CCTTAGATGG TTCTAGGGTG 1800  
GGTTTACAGC TTTTGTACT TTTACCTCCA ATAAAGGGAA AATGAAGCTT TTTATGTAAA 1860  
TTGGTTGAAA GGTCTAGTTT TGGGAGGAAA AAAGCCGTAG TAAGAAATGG ATCATATATA 1920  
TTACAACATA CTTCTTCAAC TATGGACTTT TTAAGCCTAA TGAAATCTTA AGTGTCTTAT 1980  
ATGTAATCCT GTAGGTTGGT ACTTCCCCCA AACTGATTAT AGGTAACAGT TTAATCATCT 2040  
CACTTGCTAA CATGTTTTTA TTTTCACTG TAAATATGTT TATGTTTTAT TTATAAAAAT 2100  
TCTGAAATCA ATCCATTTGG GTTGGTGGTG TACAGAACAC ACTTAAGTGT GTTAACTTGT 2160  
GACTTCTTTC AAGTCTAAAT GATTTAATAA AACTTTTTTT AAATTAAAAA AAAAA 2215

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(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: HEAONOT03
- (B) CLONE: 3088178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148 :

GGTTGACATG ATGAACAATC GGTTTCGGAA GGATATGATG AAAAATGCTA GTGAAAGTAA 60  
ACTTTCGAAA GACAACCTTA AAAAGAGACT TAAAGAAGAA TTCCAACATG CCATGGGAGG 120  
AGTACCTGCC TGGGCAGAGA CTAATAAGCG GAAAACATCT TCAGATGATG AAAGTGAAGA 180  
GGATGAAGAT GATTTGTTGC AAAGGACTGG GAATTCATA TCCACATCAA CTTCTCTTCC 240  
AAGAGGCATC TTGAAGATGA AGAACTGCCA GCATGCGAAT GCTGAACGTC CTACTGTTGC 300  
TCGGATCTCA TCTGTGCAGT TCCATCCCGG TGCACAGATT GTGATGGTTG CTGGATTAGA 360  
TAATGCTGTA TCACTATTTT AGGTTGATGG GAAAACAAAT CCTAAAATTC AGAGCATCTA 420  
TTTGAAAGG TTTCCAATCT TTAAGGCTTG TTTTAGTGCT AATGGGGAAG AAGTTTTAGC 480  
CACGAGTACC CACAGCAAGG TTCTTTATGT CTATGACATG CTGGCTGGAA AGTTAATTCC 540  
TGTGCATCAA GTGAGAGGTT TGAAAGAGAA GATAGTGAGG AGCTTTGAAG TCTCCCCAGA 600  
TGGGTCCTTC TTGCTCATAA ATGGCATTGC TGGATATTTG CATTTGCTAG CAATGAAGAC 660  
CAAAGAAGT ATTGGAAGCA TGAAAATTAA TGGAAGGGTT GCAGCATCCA CATTCTCTTC 720  
AGATAGTAAG AAAGTATACG CCTCTTCGGG GGATGGAGAA GTTTATGTTT GGGATGTGAA 780  
CTCAAGGAAG TGCCTTAACA GATTTGTTGA TGAAGGCAGT TTATATGGAT TAAGCATTGC 840  
CACATCTAGG AATGGACAGT ATGTTGCTTG TGGTTCTAAT TGTGGAGTGG TAAATATATA 900  
CAATCAAGAT TCTTGTCTCC AAGAAACAAA CCCAAAGCCA ATAAAAGCTA TAATGAACTT 960  
GGTTACAGGT GTTACTTCTC TGACCTTCAA TCCTACTACA GAAATCTTGG CAATTGCTTC 1020  
AGAAAAAATG AAAGAAGCAG TCAGATTGGT TCATCTTCCT TCCTGTACAG TATTTTCAA 1080  
CTTCCCAGTC ATTAAAAATA AGAATATTTT TCATGTTCAT ACCATGGATT TTTCTCCGAG 1140  
AAGTGGATAC TTTGCCTTGG GGAATGAAAA GGGCAAGGCC CTGATGTATA GGTTGCACCA 1200  
TACTCAGAC TTCTAAAGAG ACTATTTGAA GTCCAGTTGA GTCACAAGAG AAGCCTGTCT 1260  
TGATATATCA TCTCAGAAAC TTTCTGAAT ATGTGATAAT ATATGGAAAA TGATTTATAG 1320  
ATCCAGCTGT GCTTAAGAGC CAGTAATGTC TTAATAAACA TGTGGCAGCT TTTGTTTGAA 1380  
AAAAAAAAAA AAAGG 1395



(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2609 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT19
- (B) CLONE: 3094321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149 :

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CCCCCCATGG CACTGTCGCG GGGGCTGCCC CGGGAGCTGG CTGAGGCGGT GGCCGGGGGC 60
CGGGTGCTGG TGGTGGGGGC GGGCGGCATC GGCTGCGAGC TCCTCAAGAA TCTCGTGCTC 120
ACCGGTTTCT CCCACATCGA CCTGATTGAT CTGGATACTA TTGATGTAAG CAACCTCAAC 180
AGACAGTTTT TGTTCAAAA GAAACATGTT GGAAGATCAA AGGCACAGGT TGCCAAGGAA 240
AGTGTACTGC AGTTTTACCC GAAAGCTAAT ATCGTTGCCT ACCATGACAG CATCATGAAC 300
CCTGACTATA ATGTGGAATT TTTCCGACAG TTTATACTGG TTATGAATGC TTTAGATAAC 360
AGAGCTGCCC GAAACCATGT TAATAGAATG TGCCTGGCAG CTGATGTTCC TCTTATTGAA 420
AGTGGAACAG CTGGGTATCT TGGACAAGTA ACTACTATCA AAAAGGGTGT GACCGAGTGT 480
TATGAGTGTC ATCCTAAGCC GACCCAGAGA ACCTTTCCTG GCTGTACAAT TCGTAACACA 540
CCTTCAGAAC CTATACATTG CATCGTTTGG GCAAAGTACT TGTTC AACCA GTTGTTTGGG 600
GAAGAAGATG CTGATCAAGA AGTATCTCCT GACAGAGCTG ACCCTGAAGC TGCCTGGGAA 660
CCAACGGAAG CCGAAGCCAG AGCTAGAGCA TCTAATGAAG ATGGTGACAT TAAACGTATT 720
TCTACTAAGG AATGGGCTAA ATCAACTGGA TATGATCCAG TTAAACTTTT TACCAAGCTT 780
TTTAAAGATG ACATCAGGTA TCTGTTGACA ATGGACAAAC TATGGCGGAA AAGGAAACCT 840
CCAGTTCCGT TGGACTGGGC TGAAGTACAA AGTCAAGGAG AAGAAACGAA TGCATCAGAT 900
CAACAGAATG AACCCAGTT AGGCCTGAAA GACCAGCAGG TTCTAGATGT AAAGAGCTAT 960
GCACGTCTTT TTTCAAAGAG CATCGAGACT TTGAGAGTTC ATTTAGCAGA AAAGGGGGAT 1020
GGAGCTGAGC TCATATGGGA TAAGGATGAC CCATCTGCAA TGGATTTTGT CACCTCTGCT 1080
GCAAACCTCA GGATGCATAT TTTCAGTATG AATATGAAGA GTAGATTTGA TATCAAATCA 1140
ATGGCAGGGA ACATTATTCC TGCTATTGCT ACTACTAATG CAGTAATTGC TGGGTTGATA 1200
GTATTGGAAG GATTGAAGAT TTTATCAGGA AAAATAGACC AGTGCAGAAC AATTTTTTTG 1260
AATAACAAC CAAACCAAG AAAGAAGCTT CTTGTGCCTT GTGCACTGGA TCCTCCCAAC 1320

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CCCAATTGTT ATGTATGTGC CAGCAAGCCA GAGGTGACTG TCGGCTGAA TGTCCATAAA 1380  
GTGACTGTTC TCACCTTACA AGACAAGATA GTGAAAGAAA AATTTGCTAT GGTAGCACCA 1440  
GATGTCCAAA TTGAAGATGG GAAAGGAACA ATCCTAATAT CTTCCGAAGA GGGAGAGACG 1500  
GAAGCTAATA ATCACAAGAA GTTGTGAGAA TTTGGAATTA GAAATGGCAG CCGGCTTCAA 1560  
GCAGATGACT TCCTCCAGGA CTATACTTTA TTGATCAACA TCCTTCATAG TGAAGACCTA 1620  
GGAAAGGACG TTGAATTTGA AGTTGTTGGT GATGCCCCGG AAAAAGTGGG GCCCAAACAA 1680  
GCTGAAGATG CTGCCAAAAG CATAACCAAT GGCAGTGATG ATGGAGCTCA GCCCTCCACC 1740  
TCCACAGCTC AAGAGCAAGA TGACGTTCTC ATAGTTGATT CGGATGAAGA AGATTCTTCA 1800  
AATAATGCCG ACGTCAGTGA AGAAGAGAGA AGCCGCAAGA GGAAATTAGA TGAGAAAGAG 1860  
AATCTCAGTG CAAAGAGGTC ACGTATAGAA CAGAAGGAAG AGCTTGATGA TGTCATAGCA 1920  
TTAGATTGAA CAGAAATGCC TCTAAACAGA ACCCTCTTAC TATTTAGTTT ATCTGGGCAG 1980  
AACCAGATTG TTATGTCCTT TGTTCCAAAG GGAAAAAATT GACAGCAGTG ACTTGAAAT 2040  
GATTCTGCTC CCTTTGAAAG CATTCATTTT GCTAGAAGT TTAGACACAT TGCAGTATGC 2100  
TGTATTGAAA GTAGGAATAT AGTTTTAAAA ACCCTTTGAA CAAAGTGTGT GCATAACCAG 2160  
TCATGAGATA AAACAACACA ATGCATGTTG CCTTTTTAAT GTAAATACCC TTAGGTATCA 2220  
TTAATAGTTT CAAAATATTG TGGTTTAGTA AAGTTGATAC CTGGTTATAA ATATTATGCC 2280  
TTTATTTTTG GCTAGAAGAA GAATTATTTT TAGCCTAGAT CTAACCATT TCATACTCTT 2340  
AACTGATTGA AACAGATTCA AAGAAGTATC GAGTGCTATG CATTGAAACT TGTTTTTAAA 2400  
TGTTAGATGG CACTATGTAT ATTAATGTAA AACAATGTTA ATTTACTCAA GTTTTCAGTT 2460  
TGTACCGCCT GGTATGTCTG TGTAAGAAGC CAATTTTTGT GTATTGTTAC AGTTTCAGGT 2520  
TATTTATATT CGATGTTTTG TAAACTCAA ATAACGACTA TACTTATGGA CCAAATAAAT 2580  
GGCATCTGCA TTCTTGTTAA AAAAAAAAAA 2609

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT13
- (B) CLONE: 3115936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150 :

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CCTGAGGGAT CCACAGAGGG TCGGTCCTT GGAGGGAGGA CATGCAGTGC CACGTGCCAT 60  
GGACCAGCCA GTGGACCCCA TGGCCAGCAA GGCTGCTCCT GGGGCCAGTG GGGTGGACAG 120  
TCCCGCCAC GCAGGTGACT GAGGTGCCAG TGTGGGAATG AAAATGCGGC CTGTGCTCCT 180  
GGGCCCATGC GTCTCAGCT GCCCTTCCTC TCCAGGGAAG CCTGTGTACC TGCTACTTTT 240  
TCCCGAACAA TTCATGGTAA AAACACAAAT GGTATATGGA CAAGATACTG AATGTGGAAG 300  
AAACCTACTT GACAGTGTTG GTGAAAATAG GGCCAGGATT TCACACCCGT GAATGCTTTT 360  
TACTGAAAAG TATTTTGTGT TTTTCTCCCA GTTACAGAAT GTCTGAAGGG GACAGTGTGG 420  
GAGAATCCGT CCATGGGAAA CCTTCGGTGG TGTACAGATT TTTCACAAGA CTTGGACAGA 480  
TTTATCAGTC CTGGCTAGAC AAGTCCACAC CCTACACGGC TGTGCGATGG GTCGTGACAC 540  
TGGGCCTGAG CTTTGTCTAC ATGATTTCGAG TTTACCTGCT GCAGGGTTGG TACATTGTGA 600  
CCTATGCCTT GGGGATCTAC CATCTAAATC TTTTCATAGC TTTTCTTTCT CCCAAAGTGG 660  
ATCCTTCCTT AATGGAAGAC TCAGATGACG GTCCTTCGCT ACCCACCAA CAGAACGAGG 720  
AATCCGCCC CTTCAATCGA AGGCTCCCAG AGTTTAAATT TTGGCATGCG GCTACCAAGG 780  
GCATCCTTGT GGCTATGGTC TGTACTTTCT TCGACGCTTT CAACGTCCCG GTGTTCTGGC 840  
CGATTCTGGT GATGTACTTC ATCATGCTCT TCTGTATCAC GATGAAGAGG CAAATCAAGC 900  
ACATGATTAA GTACCGGTAC ATCCCGTTCA CACATGGGAA GAGAAGGTAC AGAGGCAAGG 960  
AGGATGCCGG CAAGGCCTTC GCCAGCTAGA AGCGGGACTG AGGCTGCCTC ACGTGTTGCA 1020  
AGAACAGTTT TGAGCCATTG TTAACAATGC CTTTTTCTT CACATAAAGT AGTTGATTAC 1080  
GAGGGAGTCA AATTTTCTTT TTA AAAAGGA GCTTCAATGA TTTGTAAGT AAATATCAGG 1140  
TTCTAGAAGA AACTGGCGCT TAAACCAAAT CGCATGGATT TCTTTTTCAG TGACGTTCAA 1200  
GTGTTTCTCA CGGATGGAAT TCTAGTCAGC TGCAGGCGGG AAGCCAGGCG GGTGGAGCCC 1260  
ATGGGAGCAA GGGCGAGTGG CCGGTCCCCG CTGTGCCAGG TGGGCAGGCA GGAGCAAGGC 1320  
CTGCGAGGGA GGAACGGGCC GCTCCCCGCC AGCCGCCTTC CCCAGCAGCC GCAGGTGGTG 1380  
CCAGCCACTC CACAGAGCCC GAGGGATGAT CTAGCCTGAT TCCTGCGTGT CCGAAAGAAC 1440  
TTAACGTTTT AAAGGTGATT GTCAAGTAAC TGTGTGGGGT TCTAATGCCA GTTTCCTAAT 1500  
TCCATCTCAC TGGAGATGTT TAAAGTTGGC CTCTATCCTA ATGACTCAA ACTTGTTCT 1560  
TAACTACCAT GATTGCTTTT GAGGGCCCGG AATTATAAAT ATATATTATA TTTAATTGT 1620  
TTGAGATTAT TTTGACACAT TTCTTTGATA CGTAGAGTGT TTTGTTTTTA ATTTAAATCT 1680  
GTCCTCATGC AACCTCCAT GAGGGGCAGC GAAGCTGGCA GGGAGCAGAC TGGCTTTGTA 1740  
GGTTCAGCAC TCGGCCCCC ACTGCGGGAG AGGCGGAACC CACTTGCATG TCAGCGTTTT 1800  
TGATTGAGA AAAGAAATAC TCTCAACGTT TTACCAAGTG ATTTTACCTC CACCTTTACT 1860

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AAAGTCTTTA CCTAAAACAT GGCAGTCGCT GGACACAGGA AAGCCCACCT TTTGTTTGGC 1920  
CTTTTCGAAA GGTGACCCAT ATTGCACAGC AGAACATCAC AGCTGTGGTC CCAGATGAGA 1980  
CACTGACATG CGAGTGAAGG CCTCTCCTCC TGGGCCCCGG GCTGCGCAGG CTCCTCACTC 2040  
TGGGCGGTGT TTCCTGTCTC AGAATTGACA CGGTGAATGC TTAGTGTCTG GATTTTCTTG 2100  
TGCCAGTGTT TACATATCTG ACATCGAGCT CCTCTAAGAG GCCACGTTC AAGCTTGTGTG 2160  
TCCCTGACCC AAGATAGCCA GTGCTGCTCC CAGGTGGTAC TTCTGGTACC GTGTTGAGAC 2220  
ACTTGGGATT CTCAGACTGT GGACAGGAGT GTTTGTCAAT TTTCATACTG TTTTCTTAAT 2280  
AAGCGCTCAG GCCTAAGGTG TGACAGGAAG TCGCACGCGC TTGGCCAGAG CACAGTGAAG 2340  
CAAAGGACTG GGTGCTGATG GATGGAGCCA CGGCGGCATC TGCCCACCCG GCCGCAGCCC 2400  
CCAGTGCCTC TCCTGGTGGT CCTCCCAGTC TAGAGGGTCA CGGCCCCCCC GCCCTCCTCC 2460  
GTCTCTGGCA AGCTGACCTT GACTAACCCA GGAATACAGG GTCATCCTCA TTCCTAAGTA 2520  
AGTCAAACAG CAAGACATGG TTTGCGCGGG TCTTTGCCGG AAGCCGGTCC TGCTGGCCAG 2580  
GTGTTTTACG TCAGCAGGGA AATGTGGCAC ACGCCCTCGA GGCATTTTAA CACTGTGCTT 2640  
CAGGAAATCT CAAGTTCCAT CTTGTGTTAG TAACGTACCC ACATTTTGCT GGAGTTAGTT 2700  
TATTAAAGAT GCCTACGGTG AACTCTCTGG CGCAGGTAA ATGCAGTTTT GAAAACCTGG 2760  
AAACATCAAA TGGAGGCGGG AAATAGGCTG GGGCCGAGCT GAGGGGCTGA ACACAGCAGT 2820  
GACCGTGGGT CAGCAGGTCG CCTGCCCAGC AGGCCCCCA GGAGAGGGCT CGGGCGCCCC 2880  
TGGCAGCCCC CATACCCCCA GGACCTGGCT CGTGAGTGCG TCTGGGTCAG GAAGAGACCT 2940  
CTCTGTGCGT CTCAGGCTGA GATGCAGATT TCTGTTTTCT AAAACTGGAA GCGACCTTGA 3000  
CGTGTATTGA AGGTGTGTGT GCCAAATGCT TCCGACGAG GTGCTGGCCT TGGTTGGTTT 3060  
CTCTCTGCCC CGTGTGGTCA TCAAGTCCTG GGGGATGTGC TCTGCCCAGC CGCCCTCGGG 3120  
GAGAGCAGCG CCGCCTCCCA TGGGGCCGTG GGGCTGCTGT TCTCACTGCA CTGGCTGAAG 3180  
CAACCCGCCA GCCTCCGTGC CCCACCCAC CCAGCACGCA CTCATTAGT CCATTGCCTT 3240  
AACACAAGCC TGATGGGGCT GTTTTCTCAC AATATAACG AATAAAGTGT CTTCTGGCCT 3300  
ACTTCTGAAT TACTTCTCAA CTGTATGGTT TGGGGAAGGG AGGGAAACCT AAAATCCCGT 3360  
CCAAATAAGT GAAATTCCTG AAGAAGTGGC TGAGTCCTAC CAGGTGGGG TTAGGGAAAT 3420  
GTTCTGGGTT CAGGCGCCCC TCCCAGGGCT GAGAAAGCGC AGCCAGGGAC AGCTTTCTGT 3480  
TCTCTCCCAG GGTGGCTAGG TTAGTATCTT ACATGACAAA AACTGAGAG TGTTCTAACT 3540  
TCTGTGCAAG CAAGTTAAT CCTGAGACTA AATCTTGGCG TTCAGACTCC CGTAGAGGTC 3600  
ATCTGTGTCC AGGCCACCC GGGCGCCGGC TCA 3633

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2018 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT13
- (B) CLONE: 3116522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151 :

TGGCTCGCTG GCCGCTCCTG GAGGCGGCGG CGGGAGCGCA GGGGGCGCGC GGCCCGGGGA 60  
 CTCGCATTCC CCGGTTCCCC CTCCACCCCA CGCGGCCTGG ACCATGGACG CCAGATGGTG 120  
 GGCAGTGGTG GTGCTGGCTG CGTTCCCCTC CCTAGGGGCA GGTGGGGAGA CTCCCGAAGC 180  
 CCCTCCGGAG TCATGGACCC AGCTATGGTT CTTCCGATTT GTGGTGAATG CTGCTGGCTA 240  
 TGCCAGCTTT ATGGTACCTG GCTACCTCCT GGTGCAGTAC TTCAGGCGGA AGAACTACCT 300  
 GGAGACCGGT AGGGGCCTCT GCTTTCCCCT GGTGAAAGCT TGTGTGTTTG GCAATGAGCC 360  
 CAAGGCCTCT GATGAGGTTT CCCTGGCGCC CCGAACAGAG GCGGCAGAGA CCACCCCGAT 420  
 GTGGCAGGCC CTGAAGCTGC TCTTCTGTGC CACAGGGCTC CAGGTGTCTT ATCTGACTTG 480  
 GGGTGTGCTG CAGGAAAGAG TGATGACCCG CAGCTATGGG GCCACAGCCA CATCACCGGG 540  
 TGAGCGCTTT ACGGACTCGC AGTTCTTGGT GCTAATGAAC CGAGTGCTGG CACTGATTGT 600  
 GGCTGGCCTC TCCTGTGTTT TCTGCAAGCA GCCCCGGCAT GGGGCACCCA TGTACCGGTA 660  
 CTCCTTTGCC AGCCTGTCCA ATGTGCTTAG CAGCTGGTGC CAATACGAAG CTCTTAAGTT 720  
 CGTCAGCTTC CCCACCCAGG TGCTGGCCAA GGCCTCTAAG GTGATCCCTG TCATGCTGAT 780  
 GGGAAAGCTT GTGTCTCGGC GCAGCTACGA ACACTGGGAG TACCTGACAG CCACCCTCAT 840  
 CTCCATTGGG GTCAGCATGT TTCTGCTATC CAGCGGACCA GAGCCCCGCA GCTCCCCAGC 900  
 CACCACACTC TCAGGCCTCA TCTTACTGGC AGGTTATATT GCTTTTGACA GCTTCACCTC 960  
 AAAGTGGCAG GATGCCCTGT TTGCCTATAA GATGTCATCG GTGCAGATGA TGTTTGGGGT 1020  
 CAATTTCTTC TCCTGCCTCT TCACAGTGGG CTCACTGCTA GAACAGGGGG CCCTACTGGA 1080  
 GGAACCCGC TTCATGGGGC GACACAGTGA GTTTGCTGCC CATGCCCTGC TACTCTCCAT 1140  
 CTGCTCCGCA TGTGGCCAGC TCTTCATCTT TTACACCATT GGGCAGTTTG GGGCTGCCGT 1200  
 CTTACCATC ATCATGACCC TCCGCCAGGC CTTTGCCATC CTTCTTTCCT GCCTTCTCTA 1260  
 TGGCCACACT GTCAGTGTGG TGGGAGGGCT GGGGGTGGCT GTGGTCTTTG CTGCCCTCCT 1320  
 GCTCAGAGTC TACGCGCGGG GCCGTCTAAA GCAACGGGGA AAGAAGGCTG TGCCTGTTGA 1380

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GTCTCCTGTG CAGAAGGTTT GAGGGTGGAA AGGGCCTGAG GGGTGAAGTG AAATAGGACC 1440  
CTCCCACCAT CCCCTTCTGC TGTAACCTCT GAGGGAGCTG GCTGAAAGGG CAAAATGCAG 1500  
GTGTTTTCTC AGTATCACAG ACCAGCTCTG CAGCAGGGGA TTGGGGAGCC CAGGAGGCAG 1560  
CCTTCCCTTT TGCCTTAAGT CACCCATCTT CCAGTAAGCA GTTTATTCTG AGCCCCGGGG 1620  
GTAGACAGTC CTCAGTGAGG GGTTTTGGGG AGTTTGGGGT CAAGAGAGCA TAGGTAGGTT 1680  
CCACAGTTAC TCTTCCCACA AGTTCCCTTA AGTCTTGCCC TAGCTGTGCT CTGCCACCTT 1740  
CCAGACTCAC TCCCCTCTGC AAATACCTGC ATTTCTTACC CTGGTGAGAA AAGCACAAGC 1800  
GGTGTAGGCT CCAATGCTGC TTTCCCAGGA GGGTGAAGAT GGTGCTGTGC TGAGGAAAGG 1860  
GGATGCAGAG CCCTGCCCAG CACCACCACC TCCTATGCTC CTGGATCCCT AGGCTCTGTT 1920  
CCATGAGCCT GTTGCAAGTT TTGGTACTTT AGAAATGTAA CTTTTTGCTC TTATAATTTT 1980  
ATTTTATTAA ATTAAATTAC TGCAGTGGAA AAAAAAAA 2018

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 942 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT13
- (B) CLONE: 3117184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152 :

CCTCCATCAG CTCGCCGCGC AGCGGCTGTA TTTGCGGCCT GTGCGAGTAG GCGCTTGGGC 60  
ACTCAGTCTC CCTGGCGGGC GACGGGCAGA AATCTCGAAC CAGTGGAGCG CACTCGTAAC 120  
CTGGATCCCA GAAGGTCGCG AAGGCAGTAC CGTTTCCTCA GCGGCGGACT GCTGCAGTAA 180  
GAATGTCTTT TCCACCTCAT TTGAATCGCC CTCCCATGGG AATCCCAGCA CTCCCACCAG 240  
GGACCCACCC CCCGCAGTTT CCAGGATTTT CTCCACCTGT ACCTCCAGGG ACCCCAATGA 300  
TTCCTGTACC AATGAGCATT ATGGCTCCTG CTCCGACTGT CTTAGTACCC ACTGTGTCTA 360  
TGTTTGAAA GCATTTGGGC GCAAGAAAGG ATCATCCAGG CTTAAAGGCT AAAGAAAATG 420  
ATGAAAATTG TGGTCCTACT ACCACTGTTT TTGTTGGCAA CATTTCCGAG AAAGCTTCAG 480  
ACATGCTTAT AAGACAACCT TTAGCTAAAT GTGGTTTGGT TTTGAGCTGG AAGAGAGTAC 540  
AAGGTGCTTC CGGAAAGCTT CAAGCCTTCG GATTCTGTGA GTACAAGGAG CCAGAATCTA 600  
CCCTCCGTGC ACTCAGATTA TTACATGACC TGCAAATTGG AGAGAAAAAG CTA CTCTCGTTA 660

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AAGTTGATGC AAAGACAAAG GCACAGCTGG ATGAATGGAA AGCAAAGAAG AAAGCTTCTA 720  
ATGGGAATGC AAGGCCAGAA ACTGTCACTA ATGACGATGA AGAAGCCTTG GATGAAGAAA 780  
CAAAGAGGAG AGATCAGATG ATTAAAGGGG CTATTGAAGT TTTAATTCGT GAATACTCCA 840  
GTGAGCTAAA TGCCCCCTCA CAGGAATCTG ATTCTCACCC CAGGAAGAAG AAGAAGGAAA 900  
AGAAGGAGGA CATTTTCGGC AGATTTCAGT GGGCCCCACTG AT 942

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2060 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LNODNOT05
- (B) CLONE: 3125156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153 :

TCCCCCCTC AGCCTCCCC CCCCCACTG GCATATGGTC CTGCCCCTTC TACCAGACCC 60  
ATGGGCCCCC AGGCAGCCCC TCTTACCATT CGAGGGCCCT CGTCTGCTGG CCAGTCCACC 120  
CCTAGTCCCC ACCTGGTGCC TTCACCTGCC CCATCTCCAG GGCCTGGTCC GGTACCCCT 180  
CGCCCCCAG CAGCAGAACC ACCCCCTTGC CTGCGCCGAG GCGCCGAGC TGCAGACCTG 240  
CTCTCCTCCA GCCCGGAGAG CCAGCATGGC GGCACCTCAGT CTCCTGGGGG TGGGCAGCCC 300  
CTGCTGCAGC CCACCAAGGT GGATGCAGCT GAGGGTCGTC GGCCGCAGGC CCTGCGGCTG 360  
ATTGAGCGGG ACCCCTATGA GCATCCTGAG AGGCTGCGGC AGTTGCAGCA GGAGCTGGAG 420  
GCCTTTCGGG GTCAGCTGGG GGATGTGGGA GCTCTGGACA CTGTCTGGCG AGAGCTGCAA 480  
GATGCGCAGG AACATGATGC CCGAGGCCGT TCCATCGCCA TTGCCCCTG CTACTCACTG 540  
AAGAACCGGC ACCAGGATGT CATGCCCTAT GACAGTAACC GTGTGGTGCT GCGCTCAGGC 600  
AAGGATGACT ACATCAATGC CAGCTGCGTG GAGGGGCTCT CCCCATACTG CCCCCGCTA 660  
GTGGCAACCC AGGCCCCACT GCCTGGCACA GCTGCTGACT TCTGGCTCAT GGTCCATGAG 720  
CAGAAAGTGT CAGTCATTGT CATGCTGGTT TCTGAGGCTG AGATGGAGAA GCAAAAAGTG 780  
GCACGCTACT TCCCCACCGA GAGGGGCCAG CCCATGGTGC ACGGTGCCCT GAGCCTGGCA 840  
TTGAGCAGCG TCCGCAGCAC CGAAACCCAT GTGGAGCGCG TGCTGAGCCT GCAGTTCCGA 900  
GACCAGAGCC TCAAGCGCTC TCTTGTGCAC CTGCACTTCC CCACTTGGCC TGAGTTAGGC 960  
CTGCCCGACA GCCCCAGCAA CTTGCTGCGC TTCATCCAGG AGGTGCACGC ACATTACCTG 1020

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CATCAGCGGC CGCTGCACAC GCCCATCATT GTGCACTGCA GCTCTGGTGT GGGCCGCACG 1080  
GGAGCCTTTG CACTGCTCTA TGCAGCTGTG CAGGAGGTGG AGGCTGGGAA CGGAATCCCT 1140  
GAGCTGCCTC AGCTGGTGCG GCGCATGCGG CAGCAGAGAA AGCACATGCT GCAGGAGAAG 1200  
CTGCACCTCA GGTTCCTGTA TGAGGCAGTG GTGAGACACG TGGAGCAGGT CCTGCAGCGC 1260  
CATGGTGTGC CTCCTCCATG CAAACCCTTG GCCAGTGCAA GCATCAGCCA GAAGAACCAC 1320  
CTTCCTCAGG ACTCCCAGGA CCTGGTCCTC GGTGGGGGATG TGCCCATCAG CTCCATCCAG 1380  
GCCACCATTG CCAAGCTCAG CATTGCGCCT CCTGGGGGGT TGGAGTCCCC GGTTGCCAGC 1440  
TTGCCAGGCC CTGCAGAGCC CCCAGGCCTC CCGCCAGCCA GCCTCCCAGA GTCTACCCCA 1500  
ATCCCATCTT CCTCCCAAAC CCCCTTTCCT CCCCCTACC TGAGGCTCCC CAGCCTAAGG 1560  
AGGAGCCGCC AGTGCCTGAA GCCCCAGCT CGGGGCCCCC CTCCTCCTCC CTGGAATTGC 1620  
TGGCCTCCTT GACCCCAGAG GCCTTCTCCC TGGACAGCTC CCTGCGGGGC AAACAGCGGA 1680  
TGAGCAAGCA TAACTTTCTG CAGGCCCATA ACGGGCAAGG GCTGCGGGCC ACCCGGCCCT 1740  
CTGACGACCC CCTCAGCCTT CTGGATCCAC TCTGGACACT CAACAAGACC TGAACAGGTT 1800  
TTGCCTACCT GGTCTTACA CTACATCATC ATCATCTCAT GCCCACCTGC CCACACCCAG 1860  
CAGAGCTTCT CAGTGGGCAC AGTCTCTTAC TCCCATTCTT GCTGCCTTTG GCCCTGCCTG 1920  
GCCCAGCCTG CACCCCTGTG GGGTGGAAT GTACTGCAGG CTCTGGGTCA GGTTCGTCTC 1980  
CTTTATGGGA CCCGACATTT TTCAGCTCTT TGCTATTGAA ATAATAAACC ACCCTGTTCT 2040  
GTGAAAAAAAA AAAAAAAAAAG 2060

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2065 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT12
- (B) CLONE: 3129120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154 :

CGGGTCCCCG GGTCTGACAG GAGCAGCCTG TGGGCACCGC GCGGTTAGTT GGAGGCGGGA 60  
GAGGGTCCGT AGCCGCGCCG CCCTGCCCCG CCATGGGCCTT CCTGTCGGAC CCGGTTTCGCC 120  
GGCGCGCGCT CGCCCGCCTA GTGCTGCGCC TCAACGCGCC GTTGTGCGTG CTGAGCTACG 180  
TGCGGGGCAT CGCCTGGTTC TTGGCGCTGG TTTTCCCGCC GCTGACCCAG CGCACTTACA 240



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TGTCGGAGAA CGCCATGGGC TCCACCATGG TGGAGGAGCA GTTTGCGGGC GGAGACCGTG 300  
CCCGGGCTTT TGGCCGGGAC TTCGCCGCC ACCGCAAGAA GTCGGGGGCT CTGCCAGTGG 360  
CCTGGCTTGA ACGGACGATG CGGTACAGTAG GGCTGGAGGT CTACACGCAG AGTTTCTCCC 420  
GGAAACTGCC CTTCCCAGAT GAGACCCACG AGCGCTATAT GGTGTCGGGC ACCAACGTGT 480  
ACGGCATCCT GCGGGCCCCG CGTGCTGCCA GCACCGAGTC GCTTGTGCTC ACCGTGCCCT 540  
GTGGCTCTGA CTCTACCAAC AGCCAGGCTG TGGGGCTGCT GCTGGCACTG GCTGCCCACT 600  
TCCGGGGGCA GATTTATTGG GCCAAAGATA TCGTCTTCCT GGTAACAGAA CATGACCTTC 660  
TGGGCACTGA GGCTTGGCTT GAAGCCTACC ACGATGTCAA TGTCAGTGGC ATGCAGTCGT 720  
CTCCCCTGCA GGGCCGAGCT GGGGCCATTG AGGCAGCCGT GGCCCTGGAG CTGAGCAGTG 780  
ATGTGGTCAC CAGCCTCGAT GTGGCCGTGG AGGGGCTTAA CGGGCAGCTG CCCAACCTTG 840  
ACCTGTCTAA TCTCTTCCAG ACCTTCTGCC AGAAAGGGGG CCTGTTGTGC ACGCTTCAGG 900  
GCAAGCTGCA GCCCGAGGAC TGGACATCAT TGGATGGACC GCTGCAGGGC CTGCAGACAC 960  
TGCTGCTCAT GGTCTGCGG CAGGCCTCCG GCCGCCCCCA CGGCTCCCAT GGCCTCTTCC 1020  
TGCGCTACCG TGTGGAGGCC CTAACCCTGC GTGGCATCAA TAGCTTCCGC CAGTACAAGT 1080  
ATGACCTGGT GGCAGTGGGC AAGGCTTTGG AGGGCATGTT CCGCAAGCTC AACCACCTCC 1140  
TGGAGCGCCT GCACCAGTCC TTCTTCTCT ACTTGCTCCC CGGCCTCTCC CGCTTCGTCT 1200  
CCATCGGCCT CTACATGCCC GCTGTCGGCT TCTTGCTCCT GGTCTTGGT CTCAAGGCTC 1260  
TGGAACTGTG GATGCAGCTG CATGAGGCTG GAATGGGCCT TGAGGAGCCC GGGGGTGCCC 1320  
CTGGCCCCAG TGTACCCCTT CCCCCATCAC AGGGTGTGGG GCTGGCCTCG CTCGTGGCAC 1380  
CTCTGCTGAT CTCACAGGCC ATGGGACTGG CCCTCTATGT CCTGCCAGTG CTGGGCCAAC 1440  
ACGTTGCCAC CCAGCACTT CCAGTGGCAG AGGCTGAGGC TGTGGTGTG ACACTGCTGG 1500  
CGATTTATGC AGCTGGCCTG GCCCTGCCCC ACAATACCCA CCGGGTGGTA AGCACACAGG 1560  
CCCCAGACAG GGGCTGGATG GCACTGAAGC TGGTAGCCCT GATCTACCTA GCACTGCAGC 1620  
TGGGCTGCAT CGCCCTCACC AACTTCTCAC TGGGCTTCCT GCTGGCCACC ACCATGGTGC 1680  
CCACTGCTGC GCTTGCCAAG CCTCATGGGC CCCGGACCCT CTATGCTGCC CTGCTGGTGC 1740  
TGACCAGCCC GGCAGCCACG CTCCTTGGCA GCCTGTTTCT GTGGCGGGAG CTGCAGGAGG 1800  
CGCCACTGTC ACTGGCCGAG GGCTGGCAGC TCTTCTTGGC AGCGCTAGCC CAGGGTGTGC 1860  
TGGAGACCA CACCTACGGC GCCCTGCTCT TCCCACTGCT GTCCCTGGGC CTCTACCCCT 1920  
GCTGGCTGCT TTTCTGGAAT GTGCTCTTCT GGAAGTGAGA TCTGCCTGTC CGGGCTGGGA 1980  
CAGAGACTCC CCAAGGACCC CATTCTGCCT CCTTCTGGGG AAATAAATGA GTGTCTGTTT 2040  
CAGCAGCTAT TTGATGCTTG TCACA 2065